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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Db 1 AATGTGGGAAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCT 60 Qy 61 guaaucaugcuugcuugccuuagccgcauuguacuugauuuugcuucu 120	/organ /strai /isola /isola /db_xr /SE COUNT 190 a 22 Parameter Query Match Best Local Similarity 7 Matches 675; Conservation	ESSION A83548 SION A83548.1 GI:6732807 WORDS Reticuloendotheliosis viru RGANISM Reticuloendotheliosis viru Viruses; Retroid viruses; retroviruses; 3-Reticuloen ERENCE 1 (bases 1 to 940) UTHORS Gabus-Darlix,C. and Darlix NOVEL INTERNAL RIBOSOME EN Patent: WO 9849334-A 05-NO GABUS DARLIX CAROLINE (FR) TURES FURES FURES FURES FOR THE CONTROL OF THE CON	42 36.2 3.9 195960 42 AC013569 43 36 3.8 16832 42 AC014255 44 36 3.8 88866 41 AC010696 45 36 3.8 114958 51 AC008356 SULT 1 3548 CUS A83548 940 bp DNA PAT 21-	## ## ## ## ## ## ## ## ## ## ## ## ##
SOURCE ORGANISM Fowlpox virus Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxviriae Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxviriae Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxviriae Avipoxvirus REFERENCE 1 (bases 1 to 4292) AUTHORS Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virus Virology 235 (2), 367-376 (1997) MEDLINE 97428585 REFERENCE 2 (bases 1 to 4292) AUTHORS Hertig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.B. TITLE Direct Submission Submitted (30-MAY-1997) Division of Animal Health, CSIRO, 5 Portarlington Road, Geelong, Victoria 3213, Australia Location/Qualifiers Source	Db 901 GTTTGTACTCGTCCTCCTCCTCCCGGCCGGGATGGG 940 RESULT 2 AF006065 LOCUS AF006065 AF006065 AF006065 AF006065 VERSION AF006065 VERSION AF006065.1 GI:2393892 KEYWORDS	721 ugguaucugauuguuggaccgucuccaagacggugauaauauaagucgugguuug : : : : : : : : : : : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : : : : :

Chordopoxvirinae;

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integrated reticuloendotheliosis virus"

CDS

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Reticuloendotheliosis virus
Reticuloendotheliosis virus
Reticuloendotheliosis virus group.
Viruses; Retroid viruses; Retroviridae; Mammalian type C
retroviruses; 3-Reticuloendotheliosis virus group.

1 (bases 1 to 578)
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2 from Patent WO9849334.
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S70398
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                                Reticuloendotheliosis virus A.

Viruses; Retroid viruses; Retroviridae; Mammalian type C

retroviruses; 3-Reticuloendotheliosis virus group.

E 1 (bases 1 to 545)

Structural genes, not the LTRs, are the primary determinants of reticuloendotheliosis virus A-induced runting and bursal atrophy 94279132

GenBank staff at the National Library of Medicine created this sequence comes from Fig. 3.

Location/Qualifiers
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$70398.1 GI:547134
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'db_xref="taxon:11636"
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70.1%; Pred. No. 3.8e-173;
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 79845] from the original journal article.

This sequence comes from Fig 1C.

Location/Qualifiers

1. .583
                                                 Isfort, R., TRETOVITUS 1
Proc. Natl.
92141243
                                                                                 virus insertion.
Gallid herpesvirus
Viruses; dsDNA virus
                                                                                     Gallid herpesvirus 2 attenuated strain JM-Hi3 reticuloendotheliosis
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(bases

dšDNA virus 1 to 583)

disease

viruses, no RNA stage; Herpesviridae.

Jones,D., Kost,R., Witter,R. and Kung,H.J. insertion into herpesvirus in vitro and in Acad. Sci. U.S.A. 89 (3), 991-995 (1992)

1. .583 /organism="Gallid herpesvırus /insertion_seq=""

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                            spleen necrosis virus.

Spleen necrosis virus

Viruses; Retroviruses; Retroviridae; Mammalian type C

Viruses; Nammalian type C virus group.

1 (bases 1 to 891)

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1%; Pred. No. 3.2e-152;
1%; Pred. No. 17;
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/db_xref="taxon:11836"
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B87 bp ss-RNA

ON Reticuloendotheliosis virus 713 proviral clone RNA.

M 22224 M10660 M16722

M22224.1 GI:209709

long terminal repeat (LTR).

Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas),

CDNA to mRNA, clone 713.

SM Reticuloendotheliosis virus

Viruses; Retroid viruses; Retroviridae; Mammalian type C

retroviruses; 3-Reticuloendotheliosis virus group.

E 1 (bases 510 to 602)

S Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J.

In viro transcription analysis of the viral promoter involved in c-myc activation in chicken B lymphomas: Detection and mapping of two RNA initiation sites within the reticuloendotheliosis virus

L J. Virol. 54, 161-170 (1985)

E 85135063

F 2 (bases 1 to 867)
    aaauguucguuggaggcgagcaucagaccacuugcgccauccaaucacgagcaaacac
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2 (bases 1 to 887)

Swift,R.A., Boerkoel,C.F., Ridgway,A., Fujita,D. and Kung,H.-J.

B-lymphoma induction by reticuloendotheliosis verseterization of a mutated chicken syncytial involved in c-myc activation

J. Virol. 61, 2084-2090 (1987)
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/db_xref="taxon:11636"
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/note="3' LTR"
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1 (bases 2 to 470)

Shimotohno, K., Mizutani, S. and Temin, H.M.

Sequence of retrovirus provirus resembles tha

transposable elements

Nature 285 (5766), 550-554 (1980)

80254544

2 (bases 1 to 1530)

O'Rear, J.J. and Temin, H.M.

Spontaneous changes in nucleotide sequence in

necrosis virus, an avian retrovirus

Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-12

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The meaning of the substitution at 739-749 is

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/codon_start=1
/protein_id="CAA24513.1"
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/db_xref="SWISS-PROT:P03342"
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GCKPHRTSKVLLASQKVNPRRPVLPSAPESPPRIRRAQFLDERPLSPAPAPPPYPEV
SAIVEDTREGQOPDSTVMTSPPHTRSGLEFGAQGPSGMYPLRETGERDMTGRPMRTYV
PFTTSDLYNWKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER
VRTESRREVRNDQGVQVTDEREIEAQFPATRPDWVGS"
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s; Pred. No. 1.7e-124;
160; Mismatches 29;
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Spleen necrosis virus (
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V01205.1 GI:61794
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1 Sim:
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shimotohno, K., Mizutani, S. and Temin, H.M.
Sequence of retrovirus provirus resembles
transposable elements
Nature 285 (5766), 550-554 (1980)
80254544
                                                                                                                                                                                                                                                                                                                                                                      Spleen necrosis virus.
Spleen necrosis virus
Viruses; Retroid viruses;
retroviruses; 1-Mammalian
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ilarity 62.8%;
Conservative 11;
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/db_xref="taxon:11836"
<1. .740
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1. .859
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/db_xref="taxon:11836"
741. .>859
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/organism="Spleen necrosis
/db_xref="taxon:11836"
199 c 214 g 201 t
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s; Pred. No. 7.3e-87;
112; Mismatches 54;
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type C virus
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John Virus S envelope g
3' long terminal repeat, c
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AF006066.1 GT.
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1 (bases 1 to 1022)

Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virology 235 (2), 367-376 (1997)

97428585

2 (bases 1 to 1022)
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Viruses; dsDNA viruses,
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                                                                                                                                           /note="3' LTR of r deletions in U3, R been duplicated." 750. .>1022 /note="ORF1"
                                /note-____/codon_start-1
/product-"putative protein"
/protein_id-"AAC58242.1"
/protein_id-"AAC58242.1"
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DNNPVSLKTFTCPSKNSIRQFIKELDLLRSLQSSEHVIKLYGYILDI"
209 c 218 g 280 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus.
                                                                                                                                                                                       /organism="Fowlpox virus"
/strain="S (Standard Vaccine strain)"
/db_xref="taxon:10261"
/note="standard vaccine strain from Cyanamid-Webster
Ltd, Castle Hill, New South Wales, Australia
integrated reticuloendotheliosis virus"
<1. .382
/gene="env"
<1. .382
                                                                                                                                                                                                                                                                                      'gene≖"env"
     17.1%;
64.2%;
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      Score 160.4; D
Pred. No. 6.8e-
53; Mismatches
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-40;
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Id and vaccine strains of fowlpox virus carry integrated lences from the avian retrovirus, reticuloendotheliosis viogy 235 (2), 367-376 (1997)
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אי virus M long אל homolog gene,
/codon_start=1
/product="protein kinase homolog"
/protein_id="AAC58236.1"
/protein_id="AAC58236.1"
/db_xref="GI:2393890"
/translation="MDIITNTTMFDIQFNDIPNIPYVDIEKPLLVYSCDSYRLYNAKY
/translation="MDIITNT"
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                                                                                                                                                                                 905. .1152
/note="remnant
1223. .2080
/note="ORF2"
                                                                                                                                                                                                                                                                   /note="ORF1"
/codon_start=1
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FIEISMORCFSIKSVTDSTVLYIENRTNRYSISTSHDKNEPYEENGIIMNNIECYFVA
CLEGSCTVNVNLGDRQISDNISESSGFLMDVNTDHVIDTKYVGLFITKIKVDAHVFYG
QNVIMFPEKNLFSQTNGPNFILYDITVQDRNVLLLITSKYIYNLCDDKYYDIFELKYL
VDNCKLPMPLIPLSKYDFTFTDLSVIKSENVKTVLSKVHTSMKSYYNNDTSLPVAVKV
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TTTGTTGAAGGCAAGCATCAGACCACTTGCAC
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il Similarity 64.6%;
137; Conservative
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The genome of fowlpox virus
J. Virol. 74 (8), 3815-3831 (
20193820
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AF198100.1
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1 /bases 1 to
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Viruses; dsDNA viruses,
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                                                                                                                                           Submitted (24-OCT-1999) Microbiology, Plum Island Center, U.S. Dept. Agriculture, Agricultural Reseabox 848, Greenport, NY 11944-0848, USA Location/Qualifiers
                                                                                                                                                                                     2 (bases 1 to 28)
Afonso, C.L., Tulma
Direct Submission
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2116. .>2
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NLLEETIYDYGEDQALKHIITNISVLLIKRCYNINEKFIMKHESIFGSTRKDTITFYK
IPRIMNKWIRSRSNNKITDIGCHIYDNTKSIIAEAMFFTMKHESIFGSTRKDTITFYK
YDGTSLPVEAIHADP"
390 c 431 g 831 t
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'note="ORF3"
                      complement(1874./gene="FPV001"
complement(1874.
/gene="FPV001"
/note="C-type lec
                                                                                        Ames,
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                                                                                     /organism="Fowlpox virus"
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/country="USA: APHIS Cent
\mes, Iowa"
                                                                             'note="virulent FPV;
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pred. No. 1.8e-38;
51; Mismatches 5
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genome.
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Research Service,
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VGFRQGIQKCEKLGSDMIGKSEEEMKALKNIWTGNDHSRFWVDNRAAASTFDPVNECA
YGTRSSVSEVPKVLTSPCSVRRYLVCKKTDNSYPTTQSSFYNQYE"
3367. .4035
3367. .4035
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/gene="FPV003"
complement(4500.
/gene="FPV003"
/note="identical 1
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GB:AF021350"
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/gene="FPV005"
complement(5221. .5589)
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/note="identical to FPV256 F
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/translation="MIVEKIAAWLLYPLCLLRCFLCATCDCIRLPCVLTRRFCKRT
ECMSETLDSLEHSCCYCCVLPLLIIREFWRRVILPTLKATCDCIRLPCVLTRRFCKRT
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ICPLAKSWCRCFCCPCEVFLRCLLFPCMMLRRMHRGRLTGVREPGAFRDSRDPARRGT
WVNDWCEDLCVWIWSPCCYVKRCIRTMCDTFTKKIFYWFIAPAGSPRMPEEPSPLSRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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TDGKTFGFSPCNATYGFVCID"
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5125. .5430
                                                                                                                                                                                  /gene="FPV006"
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/note="identica
ClOL), similar
                                                                                                                                                                                                                                                                                                               /codon_start=1
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5931. .7187
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pmo sapiens SW:Q07108"
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FKSHPFKKYNGTDVMIDTMMIQDVAFYYKHDEDIRSQVVMLEXEDYRFVMFIIIPDS
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Complement(10276. .11112)
/gene="FPV011"
complement(10276. .11112)
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8048. .8248
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complement(9123. .10190)
/gene="FPV010"
/note="Fowlpox SW:P14369, similar to Homo sapiens
GB:AB006423"
/codon start=1
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FSKVCPDEWIGYNSKCYYFTINETNWNDSKKLCDVMDSSLIRFDNIETLNFVSRYGKG
WYTEYMR"
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/forc "FEV006"
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/db_xref="taxon:11836"
/clone="pSNV(wt)"
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/note="LTR"
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/gene="FPV012"
/note="similar to procedure to
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/db_xref="GI:7271510"
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SYTPLHIAAKTGNIKIIRRLIRYGANVDKETNDGYTALLIAICTGDIKTCNVLLDEGA
NPNYVNKYGITPLVRIISYYRPTILKLLMDRGANCNQIINIGQVTYTIMEYFINLFDE
YKIPILNLVPYIIISKFKASITVNIEGFNRNIAAIAKNSRLLEVALKCKSEIAFMTTR
GIGDKSLFEICILEDIKDIDHNSFVAFLDKLIESQSNLRIYGYTMNKIIEMGRYRKEL
LCSAVRVNSCNLSSLNTEWCLLPLKGKLNILSKLNNDNIKKLILNDAIKVNNKTG"
/gene="FPV013"
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gg-09-214-124-1 perfect: core: 1 daugugggsgggguccggg. perfect: 1.0 scoring table: Gappo 10.0 c gapaxt 1.0 scarched: 31158 seqs. 123086042 residues saarched: 31158 seqs. 123086042 residues saarched: 31158 seqs. 123086042 residues saarched: 31158 seqs. 123086042 residues pocal number of hits astisfying chosen parameters: pocal number of hits chocal score distribution. pocal number of hits chocal score distribution choice parameters: pocal number of hits astisfying chocal number of hits ch	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Copyright (c) 1993 - 2000 Compugen Ltd. Copyright (c) 1993 - 2000 Compugen Ltd. Compugen Ltd. Copyright (c) 1993 - 2000 Compugen Ltd. Compugen Ltd. Copyright (c) 1993 - 2000 Compugen Ltd. Compugen Ltd. Copyright (c) 1993 - 2000 Compugen Ltd. Compugen Ltd.	us-09-214-124- Tue Aug 8 08:33:18 2000
result 1 va3778 standard; DNN; 940 BP. v3378; 1999 (first entry); send of REV-A. 5 end genomic RNA; in v3378; 1999 (first entry); send of REV-A. 5 end genomic RNA; in v3378; 1999 (first entry); send of REV-A: 5 end genomic RNA; in v3378; 1990; call of the genomic RNA; in v3378; 1990; call of the genomic RNA; in v2578; 1991; containing IEES and/or encapsidation enhancer and call of the genomic RNA; in v2578; 1991; RAUGHORA CALLANDING CONTAINED AND CONTAINED A	3.0 110000 1 X13948 3.0 1425 1 Q51156 28 3.0 3412 1 X03046 28 3.0 9237 1 V57926 28 3.0 235033 1 V57903 28 3.0 237326 1 T07329 7.8 3.0 1391 1 T07329 ALIGNMENTS	1. rng 1. rng
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?53; Mismatches 18;
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Sequence derived from the 5' end of REV-A.

KW Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;

KW type C retrovirus; internal ribosome entry site; IRES; encapsidation;

KW retroviral vector; gene therapy; ss.

Reticuloendotheliosis virus.

PN FR2762615-A1.

PN FR2762615-A1.

PD 30-OCT-1998.

PR 28-APR-1997; PR-005203.

PR 28-APR-1997; FR-005203.

PR 29-037487/04.

PI Expression vectors containing IRES and/or encapsidation enhancer -

Texpression vectors containing IRES and/or encapsidation enhancer -

Texpression vectors containing IRES and/or encapsidation enhancer -

Texpression vectors containing IRES and/or encapsidation also of escribes nucleotide sequence from the 5' end of the genomic RNA of Retrovirus other than FMLV and MOMLV of the genomic RNA of a type A (RFV-A). The specification also describes nucleotide sequence derived from all or part of the 5' end of the genomic RNA of a type C retrovirus other than Friend murine leukaemia virus (MOMLV). The 5' derived sequences are used as an internal ribosome entry site (IRES) in a vector for permitting or enhancing the encapsidation of a retroviral vector. The vectors can be used for gene therapy, production of recombinant polypeptides or production of transgenic animals.

Sequence 578 BP; 94 A; 139 C; 173 G; 173 U;
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W gene transfer; gene therapy; ss.
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AC X26109;

Chicken syncytial virus provirus REV LTR sequence.

Chicken syncytial virus provirus REV LTR sequence.

Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;

KW vaccine; chicken; LTR; long terminal repeat; ss.

Avian reticuloendotheliosis virus.

PW W09907852-Al.

18-FEB-1999; AU-008454.

PR 08-AUG-1998; AU-008454.

PR 08-AUG-1998; AU-008454.

PR (CSIR ) COMMONNEALTH SCI & IND RES ORG.

PI Boyle DB; Coupar BEH, Gould AR, Hertig C;

PR Recombinant vaccine against fowlpox virus - is free of contamination per from reticuloendotheliosis virus, used to prevent the virus occurrence in chickens

PR Recombinant vaccine against fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens can be revent the occurrence of fowlpox virus in chickens. The chickens can be revent the occurrence of fowlpox virus in chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with representation provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced.

Sequence 512 BP; 130 A; 113 C; 129 G; 140 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and those genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with the vaccine fell strains at 1 day of age. Prior vaccine and field strains of FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences x26110-115 represent FPV C molecule can comprise a FPV LTR sequence selected from the above.

Sequence 536 BP; 145 A; 115 C; 133 G; 143 T;
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Best Loc
Matches
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ggaggcgagcaucagaccacuugcgccauccaaucacgagcaaacacgagaucg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 435.4; DB 1; Pred. No. 1.5e-138; 5; Mismatches 11;
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RESULT 7
076038

ID 076038 standard; DNA; 5528 BP.

AC 076038;

AC 076038;

AC 076038;

POT 20-JUL-1995 (first entry)

Retrovirus; vector; pP0111-R1; spleen necrosis virus; SNV;

KW Retrovirus; vector; pP0111-R1; spleen necrosis virus; SNV;

KW cytomegalovirus; CKW; intermediate-early promoter; IE promoter;

KW long terminal repeat; LTR; encapsidation; gene transfer;

OS Spleen necrosis virus.

PD 20-DEC-1994.

PP 07-JUN-1993; US-073345.

PP 07-JUN-1993; US-073345.

PP 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1994; DESEY.

PR 07-JUN-1993; US-073345.

PR 07-JUN-1993;
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Best Local Similarity 62.4%;
Matches 397; Conservative 1
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Pred. No. 2.8e-136;
.69; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                Length
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RESULT 8
Q76039
ID Q76039;
AC Q76039;
DT 20-JUL-1995 (first entry)
DE Retrovirus vector pP0111-R2.
KW Retrovirus; vector; pP0111-R2; spleen necrosis virus; SNV;
KW cytomegalovirus; CMV; intermediate-early promoter; IE promot
KW long terminal repeat; LTR; encapsidation; gene transfer;
Gene therapy; ss.
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                                                                 Query Match
Best Local Sin
Matches 386;
                                                                                                          W long terminal repeat; LTR; encapsidation; gene transfer;
W gene therapy; ss.
Spleen necrosis virus.
N W09429437-A.
D 22-DEC-1994.
D 27-JUN-1994; U06415.
R 07-JUN-1993; US-073345.
R 07-JUN-1993; US-073345.
R 07-JUN-1993; US-073345.
D DORNDURG RC;
IN DORNDURG RC;
IN RECOMBINANT retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect recombinant retrovirus provirus
Example; Page 14-16; 28pp; English.
C New recombination-free, highly efficient retroviral vectors peoill-R1 (given in Q76038), pp0111-R2 (Q76039) and pp0111-R3 (Q76040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV, and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of Gownstream activation of cellular proto-oncogenes.
Sequence 5525 BP; 1264 A; 1422 C; 1457 G; 1382 T;
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                                                               7%; Score 420; DB 1; 1
7%; Pred. No. 9.9e-133;
166; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1287
                                                                                    Length 5525;
                                                               Indels
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                                                               Gaps
                       730
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Recombinant retrovirus vector, contg. non-retroviral gene, - has bility to produce progeny virus, in helper cell which can infect host cell and form provirus

Example; Page 16-17; 28pp; English.

C New recombination-free, highly efficient retroviral vectors

C pPO111-R1 (given in Q76038), pPO111-R2 (Q76039) and pPO111-R3

C (Q76040) were obtained by replacing the U3 region of the left

C LTR of spleen necrosis virus with the IE promoter/enhancer of CMV

C and extension of the encapsidation region. The vectors allow

C cell-type specific gene expression and eliminate risks of

downstream activation of cellular proto-oncogenes.

Sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T:
                                                                                                                                                                                                                              Retrovirus vector pPO111-R3.

Retrovirus; vector; pPO111-R3; spleen necrosis virus; SN Retrovirus; vector; pPO111-R3; spleen necrosis virus; SN cytomegalovirus; CMV; intermediate-early promoter; IE proceed therapy; ss.

Vector of the second second the s
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Q76040;
20-JUL-1995
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                                                    20-MAY-1999 (first entry)
Fowlpox virus (FPV S3') LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus vaccine; chicken; LTR; long terminal repeat; ss.
Fowlpox virus.
W09907852-A1.
18-FEB-1999.
07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
Boyle DB, Coupar BEH, Gould AR, Hertig C;
WPI; 99-167428/14.
Recombinant vaccine against fowlpox virus - is free of confront reticuloendotheliosis virus, used to prevent the virus from reticuloendotheliosis virus, used to prevent the virus.
                             occurrence in Claim 18; Fig
                                                                                                                                                             X26111 stand
X26111;
20-MAY-1999
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18; Fig 5; 127pp; English.
18; Fig 5; 127pp; English.
19 produce a vaccine against fowlpox virus (FPV) whose nucleic genome does not contain any REV sequence. The recombinant FPV is to produce a vaccine against fowlpox virus. The vaccine is used to the occurrence of fowlpox virus in chickens. The chickens can be
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DT 20-MAY-1999 (first entry)
DE Fowlpox virus (FPV S) 3' LTR sequence.

KW Powlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
KW vaccine; chicken; LTR; long terminal repeat; ss.

FOWLpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
KW vaccine; chicken; LTR; long terminal repeat; ss.

PN vaccine; chicken; chicken
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X2611
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AZ X26112 standard; DNA; 298 BP.

AZ X2612;

DT 20 MAY-1999 (first entry)

DE Fowlpox virus (FPV M3) LTR sequence.

KF Fowlpox virus; FPV, recombinant; reticuloendotheliosis virus; REV;

KW vacchie; chicken; LTR; long terminal repeat; SS.

Powlpox virus

Powlpox virus

POW 1007-872-41.

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Pred. No. 2e-43;
51; Mismatches !
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PF 07-AUG-1998; AU0628.

PF 07-AUG-1998; AU0628.

PF 08-AUG-1997; AU-008454.

PR 08-AUG-1998; AU0628.

PR 07-AUG-1998; AU0628.

PR 07-AUG-1998; AU0628.

PR 08-AUG-1997; AU-008454.

PR 08-AUG-1997; AU-008454.

PR 08-AUG-1997; AU-008454.

PR 10-1997; AU-008454.

PR 10-1998; AU0628.

PR 10-1997; AU-008454.

PR 10-1998; AU0628.

PR 10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.6%;
Best Local Similarity 64.6%;
Matches 137; Conservative
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X26114;
20-MAY-1999
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Fowlpox virus (FPV M3) LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis vaccine; chicken; LTR; long terminal renowther.
                 X18925 stand
X18925;
12-MAY-1999
Phaseolus lu
Phaseolus lu
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 Phaseolus
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                                      lunatus
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ADA2 trai
                      ADA2;
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                    transcription action transcription action
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                                                                                              ВP
                    adapter en
on adapter;
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                                        encoding cDNA.
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                         herbicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding plant ADA2 transcription activator - used for regulating expression of genes in plants and to screen for specific inhibitors, potentially useful as herbicides of the present sequence encodes the ADA2 transcription adapter isolated of the present sequence encodes the ADA2 transcription adapter isolated from Phaseolus lunatus. Also described are chimeric genes comprising the ADA2 nucleic acid sequence operably linked to suitable regulatory the ADA2 nucleic acid sequence operably linked to suitable regulatory calter the expression level of a homologue of the yeast ADA2 protein, alter the expression level of a homologue of the yeast ADA2 protein, are normally regulated by ADA2, using antisense or co-suppression contects are normally targeted by factors with which ADA2 interact; and (ii) to compound that inhibit ADA2, potentially useful as herbicides. Fragments of the ADA2 nucleic acid sequence (or synthetic primers based on it) are used in hybridisation screens to obtain sequences encoding companing genes (e.g. for plant breeding) or to identify loss of function mapping genes (e.g. for plant breeding) or to identify loss of function cutant phenotypes.
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Best Local
Matches 4
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28-JAN-1999.
15-JUL-1998;
18-JUL-1997;
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mutant pheno
Sequence 1
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Liu Z;
WPI; 99-
P-PSDB;
                                                                                                                                                                                                             V74552; tandard; DNA; 5000 BP.

V74552;
16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #241.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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7; US-897175.
PONT DE NEMOURS
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1812 BP;
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                                                                          a "these bases represent a line of missing text the sequence listing in the specification. The are included to maintain the nucleotide number of the specification for this DNA sequence."
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
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Search completed: August Job time: 445 sec
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PT Polynucleotide(s) and proteins derived from Staphylococcus aureus of stored on computer readable medium and used in the production of proteins at the invention. The DNA sequences are recorded on a computer readable medium and used in the production of protein sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access the S. aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or clikely to encode antigens have been identified and these polypeptides can also be used in a vaccine composition against S. aureus infection of S. aureus in a sample. S. aureus in fection of S. aureus in a sample. S. aureus in fection of S. aureus in a sample. S. aureus in singulative polypeptides can be used in a kit for the immunodetection of S. aureus in a sample. S. aureus infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences of any of the S. aureus DNA sequences contained on the computer readable medium.

Sequence 5000 BP; 1377 A; 990 C; 641 G; 1808 T;
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Best Local S
Matches 21
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30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, F.
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Similarity 29.2%;
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
US-08-232-463-14
US-08-793-599-1
US-08-687-080-105
US-08-687-080-105
US-09-226-568-18
US-09-2211-640-1
US-09-211-640-1
US-08-068-945A-1
US-08-068-945A-1
US-08-222-177A-17
US-08-222-177A-52
US-08-323-170B-1
US-08-162-081B-34
US-08-780-872-34
US-08-780-872-32
US-08-724-394A-20
US-08-724-394A-21
US-08-261-662-1
PCT-US95-07752-1
US-08-843-530B-1
US-09-010-398-14
US-09-010-398-14
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US-08-232-463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-9300
TELEFAX: (703)836-9300
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONF: PT7GPT+-F1c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION
SEQUENCE C
LENGTH:
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US-07-842-349-1
US-08-676-967-2
US-08-676-974-2
US-08-676-974-2
US-09-098-487-2
US-08-781-802-11
US-08-781-802-9
US-08-731-722-1
US-08-731-722-1
US-08-731-722-3
US-08-731-722-3
US-08-731-722-3
US-08-731-722-3
US-08-731-722-1
US-08-731-802-1
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US-08-731-722-1
US-08-731-802-1
US-08-731-802-1
US-08-731-802-1
US-08-731-802-1
US-08-937-271-12
US-08-937-271-12
US-08-937-271-15
US-08-164-614A-1
US-08-164-614A-1
US-08-456-489B-1
PCT-US93-01720-1
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US-08-793-599-1/c
                                                                                                                                                                                                                                                                                                                APPLICANT: ITO, KAZUTOSHI

APPLICANT: KIHARA, MAKOTO

TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER

FILE REFERENCE: 2589-0056-0 PCT

CURRENT APPLICATION NUMBER: US/08/793,599

CURRENT FILING DATE: 1997-03-04

EARLIER APPLICATION NUMBER: PCT/JP96/01866

EARLIER FILING DATE: 1996-07-05

EARLIER APPLICATION NUMBER: JP 191028/1995

PARLIER FILING DATE: 1995-07-05

NUMBER OF SEQ ID NOS: 3
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Best Local
Matches 2
                                           3-08-793-599-3/c
Sequence 3, Application
Patent No. 5952489
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: OKADA, YU
APPLICANT: YOSHIGI,
APPLICANT: ITO, KAZU
APPLICANT: KIHARA, M
                                   GENERAL
                        APPLICANT:
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application Patent No. 5952489
                                                                                                                                                                                                                                                                                                        NUMBER OF SOFTWARE:
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08-793-599-
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Best Local
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                                                                                                                                                                                                                                                                                    LENGTH: 1276
                                                                                                                                  790
                                                                                                                                                       136
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INFORMATION:
ANT: OKADA, YUKIO
ANT: YOSHIGI, NAOHIR
ANT: ITO, KAZUTOSHI
                                                                                                           GTTTCCTTAATTTATTTCATGCCTT
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ATTAATGTTCAAACGTGTCCACTAGAGTTCAAGTCTCAGACTTGACATTTGTGTTTGCAA 77
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| Similarity 4.5%;
| 13; Conservative 1
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           NAOHIRO
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; SOFTWARE: Pate
; SEQ ID NO 3
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Bar
US-08-793-599-3
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US-08-687-080-105/c
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FILE REFERENCE: 2589-0056-0 PCT

CURRENT APPLICATION NUMBER: US/08/793,599

CURRENT FILING DATE: 1997-03-04

EARLIER APPLICATION NUMBER: PCT/JP96/01866

EARLIER FILING DATE: 1996-07-05

EARLIER APPLICATION NUMBER: JP 191028/1995

EARLIER FILING DATE: 1995-07-05

EARLIER FILING DATE: 1995-07-05

NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10
Patent No.
GENERAL II
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Best Local
Matches 2
                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, 1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 CLASSIFICATION: 435
PRIOR APPLICATION: 435
                          TELEFAX:
INFORMATION FO
                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
SEQUENCE CHAR
LENGTH: 13
                                                                                                                         APPLICATION
FILING DATE
ATTORNEY/AGEN
                                                                      TELECOMMUNIC
         REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
FORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
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CITY: 1
STATE:
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                                                                                                                NAME:
                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94306
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5. 5965427
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Similarity 27.1%;
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                                                                                                                      CATION DATA:
ON NUMBER: US 08,
TE: 26-JAN-1996
ENT INFORMATION:
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ON NUMBER:
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Cambridge Avenue,
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Avenue, Suite 250
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Pred. No. 1.9;
28; Mismatches
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                                                                                                                                                                                                                                    Version
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MOLECULE TYPE: HYPOTHETICAL:

DNA NO

(genomic)

LENGTH: 13158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOI
; INDIVIDUAL ISOI
US-08-687-080-105
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US-09-226-568-18/c
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US-08-077-848A-1/c
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Matches
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Best Loc
Matches
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Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                    Sequence 1, Application US/08077848A Patent No. 5470955
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
                                                                                                   TITLE OF INVENTION: ANT
TITLE OF INVENTION: ANT
TUBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spenslev T
STREET: 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10896
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
CURRENT
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                                                                                                                                                                                                                                                                                                                887
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Local Similarity 34.0%;
les 18; Conservative
      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                           CITY: Los Angeles
STATE: California
                                                                    COUNTRY: USA
ZIP: 90067
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Similarity 56.2%;
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; LOCATION:
; OTHER INF
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US-08-077-848A-1
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 27
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Patent No.
GENERAL IN
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                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, VO

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/211,640

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: PD-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5110

TELEFAX: (619) 455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                              NUMBER OF SEC
CORRESPONDENC
ADDRESSEE:
STREET: 18
CITY: Los
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FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/077,848A FILING DATE: 16-JUN-1993 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE
                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                    ATTORNEY/F
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                                                                                                 APPLICATION NUMBER: FILING DATE:
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27;
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Craig, Ruth W.
INVENTION: ANTIBODIES WHICH
INVENTION: POLYPEPTIDE
SEQUENCES: 4
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N: 61.1110
NFORMATION:
NFORMATION:
NFORMATION:
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California
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milarity 56.28;
Conservative
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E: Spensley Horn Jubas &
1880 Century Park East,
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                                                                                                                                                                        US/09/211,640
                                                                                                                08/441,375
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Pred. No. 11;
9; Mismatches
                                            PD-2845
                                                                                                                                                                                                                                                                                                                               Suite 500
                                                                                                                                                                                                    Version
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; NAME/KEY: CDS; LOCATION: 61..1110; OTHER INFORMATION: 6; OTHER INFORMATION: 6; OTHER INFORMATION: 6US-09-211-640-1
                                                                                                                                                 COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03547
FILING DATE: 31-MAR-1994
CLASSIFICATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
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PCT-US94-03547-1/c
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LOCATION: 61..1110
OTHER INFORMATION: /
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                                                                                                                     LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
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TITLE OF INVENTION: MYELOID C
TITLE OF INVENTION: MCL-1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STREET: 18
CITY: Los
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TOPOLOGY: li
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California
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ilarity 56.2%;
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acid 227 =
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RESULT 9
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FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)819-8783
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1.
Patent No.
GENERAL II
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Matches
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COMPUTER READAB
MEDIUM TYPE:
COMPUTER: IB
OPERATING SYS
SOFTWARE: Pa
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
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PRIOR APPLICATION DATA:
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                                        TISSUE TYPE:
                                                                                              TOPOLOGY:
                                                          ORGANISM:
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Similarity 56.2%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: United States 10036-2787
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1155 Avenue of the
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6483
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Tornell,
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Hansson, I
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CDS
join(1653..1727,
                                                      Homo sapiens
                                                                                                  linear
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27-MAY-1993
N: 435
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                                         Mammary
                                                                                  DNA (genomic)
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                                          gland
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Pred. No. 1
4071..4221, 4307..4429, 4707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Americas
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
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RESULT 10
US-08-442-806-1
                                                                                                                               Query Match
Best Local Sir
Matches 51;
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LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11391)
OTHER INFORMATION: /EC_number= 3.1.1.1
OTHER INFORMATION: /product= "Bile Salt-Stimulated Finance"
FEATURE:
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LOCATION:
FEATURE:
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Pred. No. 21;
4; Mismatches
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10124..10321, 10650..11394)
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Sequence 1, Application Patent No. 5716817
GENERAL INFORMATION:
APPLICANT: Bjurse
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INFORMATION
SEQUENCE C
LENGTH:
TYPE:
TYPE:
TYPE:
TOPOLOGY
MOLECULE T
ORIGINAL S
                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEPHONE: (212)819-8783
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
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ZIP: 10
COMPUTER RI
MEDIUM TO
COMPUTER
COMPUTER
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NUMBER OF SEQ
CORRESPONDENC
ADDRESSEE:
               NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TISSUE T
FEATURE:
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CITY: 1
STATE:
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10036-2787
READABLE FORM:
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PEDNESS: dominion
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SEQUENCES: 58
VDENCE ADDRESS:
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                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                           TYPE:
Y: mat_peptide
N: join(1722..1727, 4071..4221, 4307..4429, 4707
N: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
N: ..8521, 8719..8922, 10124..10321, 10650..11391)
NFORMATION: /EC_number= 3.1.1.1
                                                                                                                                                                                                        SOURCE:
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Enerback,
Hansson, L
Lidberg, U
Nilsson, J
Tornell, J
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join(1653..1727, 4071..4221, 4307..4429, 4707
..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
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Jeanette
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Peter
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RESULT 11
US-08-222-177A-17
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; LOCATION:
US-08-442-806-1
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Best Local S
Matches 51
                                          Sequence 17, Application Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, Janittle OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                            7227
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LOCATION:
FEATURE:
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NAME/KEY:
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  ADDRESS:
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(dC-dA)n.(dG-dT)n SEQUENCES
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Pred. No. 21;
4; Mismatches
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TELEPHONE: (608) 831-210
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Cauc
TISSUE TYPE: Blood
                                                                                                                                                                                                                                                                                                                    LOCATION: 72..91
IDENTIFICATION METHOD: e: OTHER INFORMATION: /evide OTHER INFORMATION: /stance OTHER INFORMATION: /citate FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                   OTHER OTHER FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION:
                                                                                  NAME/KEY: misc_feature
LOCATION: 1..221
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPER:
OTHER INFORMATION: /standard_name=
PUBLICATION INFORMATION:
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NAME/KEY:
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CHROMOSOME/SEGMENT:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: repeat_reconstantion: 103..139
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                 AUTHORS:
AUTHORS:
TITLE: D
                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: complement (144..163)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
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            Weber, J. L.
May, P. E.
Dinucleotide repeat p
D3S240 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE:
Nucleic Acids Res
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/citation= ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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/evidence= EXPERIMENTAL
/---dard_name= "PCR primer"
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                                                                                                       strand sequenced"
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RESULT 12
US-08-222-177A-52
; Sequence 52, Application US/08222177A
; Patent No. 5582979
; Patent No. 5582979
· GENERAL INFORMATION:
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; PAGES: 388-396
; DATE: 1989
US-08-222-177A-17
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Best Loc
Matches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison
STATE: Wisconsin
COUNTRY: USA
                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 278 base pair:
                                                                                                                       ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 0986

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 831-2106

TELEFAX: (608) 831-2106
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FO
MEDIUM TYPE: Flo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Weber, James
AUTHORS: May, Paula E
TOPOLOGY:
MOLECULE TYPO
ORIGINAL SOL
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                         LENGTH: 278 base pairs TYPE: nucleic acid STRANDEDNESS: double
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28; Conservative
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 TYPE:
SOURCE:
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Pred. No. 3.3;
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NAME/KEY:
LOCATION:
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PUBLICATION :
AUTHORS: 1
AUTHORS: 1
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CHROMOSOME/SEGMENT:
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LOCATION: 20..39 \
LOCATION: 20..39 \
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
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IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
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S: Kwitek, A. E.
S: Xiao, H.
S: McPherson, J. D.
S: Wasmuth, J. J.
S: Wasmuth, J. J.
polymorphisms
                                                                                                                    3.0%; Score 28.2; DB imilarity 30.5%; Pred. No. 3.8; Conservative 25; Mismatches
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May, Paula E.

Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
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ISOLATE: Caucasian
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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RESULT 13 US-08-323-170B

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RESULT 14
US-08-162-081B-34
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Best Local S
Matches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: UP
FILING DATE: 13-OCT-11
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP
FILING DATE: 29-JAN-11
                             APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhapplicant: Bala; Waterfield, Michael Derek; Parker, APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George APPLICANT: Stefano; Gout, Ivan Tarasovitch TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITIE OF INVENTION: THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and T
STREET: Two Embarcadero C
CITY: San Francisco
STATE: California
              NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Williamson, Kim C. APPLICANT: Kaslow, David C. TITLE OF INVENTION: Cloning and TITLE OF INVENTION: faliciparum NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                            396
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APPLICANT: Willia
APPLICANT: Kaslow
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larity 31.5%;
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13-OCT-1994
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29-JAN-199
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                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08780872
Patent No. 5846824
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/GB93/00 FILING DATE: 13 APril 1993 ATTORNEY/AGENT INFORMATION: NAME: Pasqualini, Patricia A. REGISTRATION NUMBER: 34,894 REFERENCE/DOCKET NUMBER: LUD 52 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200 TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS: LENGTH: 3240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION
                                                                                                                                                                                               TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Felfe &
                      COMPUTER:
OPERATING
SOFTWARE:
CURRENT APPL
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FILING DATE: February
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO
FILING DATE: 13 April
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
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CITY: New Y
STATE: New
COUNTRY: US
ZIP: 10022
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IRRENT APPLICATION DATA:
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TOPOLOGY: 11
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SYSTEM: PC-DO
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February 7, 1994
ON: 435
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATRICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
US-08-780-872-34
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Search completed: August Job time: 870 sec
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em_est119: *
em_est110: *
gb_est2: *
gb_est4: *
gb_est11: *
gb_est12: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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Direct Submission
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15C20"
/note="end : SP6"
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S Genoscope.

Direct Submission

L Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN17J04"
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Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15017"
/note="end : T7"
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
     CNS016VI 995 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16K15 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL107256
AL107256.1 GI:5626409
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16C05"
/note="end: SP6"
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Submitted (23-JUL-1999) Genoscope
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16K15"
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segref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Buchetcand Genevieve Payan. It has been constructed in the vector
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Location/Qualifiers

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fruit fly.
Drosophila melanogaster
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Pterygota; Neoptera; Endopterygo
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencay BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns. - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part o collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL065629
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as parcollaboration with the Berkeley Drosophila Genome Project (BD)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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                                                                                                                                 Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa Aaron Mammoser in Pieter de Jong's laboratory in the Depare
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Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC
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Drosophila melanogaster
Submitted (23-JUL-1999) Genoscope - Centre National de Sequence BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cn - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MI
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta,
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Ism Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Direct Submission Survey sedex - FRANCE (E-mail: seqref@genoscope.

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

Collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Ecorl digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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fruit fly.
Drosophila
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Direct Submission
Submitted (23-JUL-1999) Genoscope
BP 191 91006 EVRY cedex - FRANCE (
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/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone-"BACN05C05"
/note-"end : T7"
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachyc
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15017"
/note="end : T7"
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/db_xref-"taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15C20"
/note="end : Sp6"
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S Genoscope.

Direct Submission

L Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16C05"
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fruit fly.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexal
Pterygota; Neoptera; Endopterygota; Diptera; Br
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/db_xref="taxon:7227"
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Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03M12"
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(E-mail : segref@genoscope.cns.fr
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E 1 (bases 1 to 937)

E 2 (bases 1 to 937)

E 3 Genoscope.

Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY Cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Insert Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's
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segref@genoscope.cns.fr
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CNS006ON 910 bp DNA GSS 03-JUN-1999

ON Drosophila melanogaster genome survey sequence T7 end of BAC # fly), genomic survey sequence.

AL065629

fruit fly.

AL065629.1 GI:4944698

GSS.

fruit fly.

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 910)

Is Genoscope.

Direct Submission

Submitted (02-UN-1999) Genoscope - Centre National de Sequencage: Web: www.genoscope.cns.fr

Petermination of this BAC-end sequence was carried out as part of a please see http://www.fruitily.org The BDGP Drosophila

melanogaster genome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
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Similarity 3.4%;
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fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins

Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Drosophila.

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 977)
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L Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre Centre Nation of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - Centre National Centre Na
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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ND Drosophila melanogaster genome survey sequence T7 end of BA
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fly), genomic survey sequence.

AL106675

AL106675.1 GI:5623167

GSS.

fruit fly.
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insect.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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            - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheta and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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FILE REFERENCE: 2589-0056-0 PCT
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CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER FILING DATE: 1996-07-05
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RESULT 4
US-08-687-080-105/c
; Sequence 105, Appl.
; Patent No. 5965427
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; ORGANISM: Barley
US-08-793-599-3
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ITTLE OF INVENTION: TISSUE-SPECIFIC PROMOTER

FILE REFERENCE: 2589-0056-0 PCT

CURRENT APPLICATION NUMBER: US/08/793,599

CURRENT FILING DATE: 1997-03-04

EARLIER APPLICATION NUMBER: PCT/JP96/01866

EARLIER FILING DATE: 1996-07-05

EARLIER APPLICATION NUMBER: JP 191028/1995

EARLIER FILING DATE: 1995-07-05

NUMBER OF SEQ ID NOS: 3
                                    PRIOR APPLICATION 455
APPLICATION NUMBER: US 08/592
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 13158 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATE: 1992
EARLIER FILING DATE: 1992
NUMBER OF SEQ ID NOS: 3
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Best Local
Matches 2
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TITLE OF IN
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COMPUTER RE
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CORRESPONDE
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
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APPLICATION NO...

FILING DATE: 17-JUL-15

CLASSIFICATION: 435

CLASSIFICATION DATA:

TMRER: U!
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                           LENGTH: 13158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
COMPUTER: I
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OF INVENTION: Human R
R OF SEQUENCES: 175
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Similarity 27.1%;
3; Conservative 2
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YPE:
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              linear
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) Cambridge Avenue, Suite
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N: 435
DNA.
(genomic)
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Pred. No. 1.4;
28; Mismatches
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RESULT 5
US-09-226-568-18/c
; Sequence 18, Appl
; Patent No. 600199
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US-08-077-848A-1/c
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OTHER INFORMATION:
US-09-226-568-18
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Best Local S
Matches 27
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Best Local S
Matches 18
                                                                                                                                                                                            Sequence 1, Application US/08077848A Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Pate
SEQ ID NO 18
LENGTH: 3934
TYPE: DNA
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                         TITLE OF INVENTION: ANT
TITLE OF INVENTION: ANT
TITLE OF INVENTION: POL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Ho
STREET: 1880 Century Pol
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER RF**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo FEATURE:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                              525
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Similarity 34.0%;
18; Conservative
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20; Mismato
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k East,
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; OTHER IN ; OTHER IN US-08-077-848A-
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US-09-211-640-
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Best Local S
Matches 27
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TELEFAX: (
INFORMATION FOR
SEQUENCE CHAR
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/077,848A FILING DATE: 16-JUN-1993 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: PD-2845 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100 TELEPHONE: (619) 455-5110 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
ATTORNAL
                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 90067
COMPUTER READABL:
MEDIUM TYPE:
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MOLECULE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: FEATURE:
                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley
STREET: 1880 Century
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF
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LOCATION:
OTHER INFO
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STRANDEDNESS: single
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ON: 61..1110
INFORMATION:
INFORMATION:
INFORMATION:
A-1
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                                                                                                                                                                                                                                                                                                                                                                                              : Craig, Ruth W.
INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
INVENTION: POLYPEPTIDE
SEQUENCES: 4
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imilarity 56.2%;
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                                                                                                                                  08/441,375
                                                                                                                                                                                           US/09/211,640
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Suite 500
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Query Ma Best Loc Matches

Local

5.0%; Similarity 56.2%; 27; Conservative

Score 28.8; DE Pred. No. 8.1; 9; Mismatches

DB

9

Length 3946;

12;

Indels

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Gaps

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OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: a.
COTHER INFORMATION: a.
PCT-US94-03547-1
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PCT-US94-03547-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-211-640-1
                                                                                                                                                                NAME: Wetherell, Jr., Ph.D., J
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application GENERAL INFORMATION:
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Best I
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                                                                                                                     TYPE: nucleic a
STRANDEDNESS: :
TOPOLOGY: linea
MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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LOCATION: 61..1110
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: 1
STATE:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/03547 FILING DATE: 31-MAR-1994 CLASSIFICATION:
                                                                                                 CLONE:
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RESULT 9
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                                                                                                                                                           APPLICATION NUMBER: US/08/068,945A
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base Dairs
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Patent No.
GENERAL II
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                          MOLECULE TY
ORIGINAL SC
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CORRESPONDENC
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STRANDEDNESS: don't
TOPOLOGY
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STREET: 1
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STATE:
                                                        ORGANISM
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RY: United States
10036-2787
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4071..4221, 4307..4429, 4707
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FEATURE:

NAME/KEY:

LOCATION:

LOCATION:

US-08-068-945A-1
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Best Local S
Matches 51
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LOCATION:
FEATURE:
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LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11391)
OTHER INFORMATION: /EC_number= 3.1.1.1
OTHER INFORMATION: /product= "Bile Salt-Stimulated Identification" | FEATURE:
                                            7167
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8719..8922,
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RESULT 10 US-08-442-806-1

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TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION ATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: SE 9202088-2
PRIOR APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base Dairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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OF INVENTION: (
LITLE OF INVENTION: E
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: White
STREET: 115°
CITY: No
                                                                                            NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
FEATURE:
                                                                                                                                                                                TISSUE FEATURE:
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ORIGINAL
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                               NAME/KEY:
LOCATION:
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COUNTRY
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SEE: White & Case
: 1155 Avenue of to
New York
                                                                                                                                                                                              TYPE:
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Y: mat_peptide
N: join(1722..1727, 4071..4221, 4307..4429, 4707
N: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
N: ..8521, 8719..8922, 10124..10321, 10650..11391)
NFORMATION: /EC_number- 3.1.1.1
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: United States
0036-2787
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Carlsson,
Enerback,
Hansson, L
Lidberg, U
Nilsson, J
                                                                                                         CDS

join(1653..1727, 4071..4221, 4307..4429, 4707

..4904, 6193..6323, 6501..6608, 6751..6868, 8335

..8521, 8719..8922, 10124..10321, 10650..11394)
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; NAME/KEY:
; LOCATION:
US-08-442-806-1
                                         US-08-222-177A-17

; Sequence 17, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.
                                                                                                RESULT
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Best Local
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LOCATION:
FEATURE:
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   CORRESPONDENC
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Similarity 33.6%;
51; Conservative
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T: Weber, James
'INVENTION: LEI
'INVENTION: (de
)F SEQUENCES: 4
)NDENCE ADDRESS:
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         James L.

: LENGTH POLYMORPHISMS
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TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..221
IDENTIFICATION METHOD: e
OTHER INFORMATION: /eyid
OTHER INFORMATION: /stan
PUBLICATION INFORMATION:
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TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Homo
INDIVIDUAL ISOL
TISSUE TYPE: B
IMMEDIATE SOURCE:
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CLASSIFICATION APPLICATION AP
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NAME/KEY:
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LOCATION: 103..139
OTHER INFORMATION: /rpt_t
OTHER INFORMATION: /rpt_t
OTHER INFORMATION: /citat
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IDENTIFICATION METHOD: 6
OTHER INFORMATION: /evic
OTHER INFORMATION: /star
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                                                                                              AUTHORS:
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Weber, J. L.
May, P. E.
Dinucleotide repeat F
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Nucleic Acids Res.
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VICATION INFORMATION:
VE: (608) 831-2100
(608) 831-2106
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)RMATION: /standard_name= "Only
INFORMATION:
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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/evidence= EXPERIMENTAL
/standard_name= "PCR primer"
/citation= ([1])
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/evidence= EXPERIMENTAL
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RESULT 12
US-08-222-177A-52
; Sequence 52, Application; Patent No. 5582979
; Patent No. 5582979
; Patent INFORMATION: Weber, Compared to the second control of the second contro
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; DATE: 1989
US-08-222-177A-17
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Best Loc
Matches
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 278 base pairs
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
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TITLE OF INVENTION: LENG
TITLE OF INVENTION: (dc.
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross
 ORIGINAL
                      MOLECULE
                        nucleic acid
STRANDEDNESS: double
TOPOLOGY: line
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AUTHORS:
TITLE: A
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28; Conservative
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TYPE:
SOURCE:
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ER: 09865.601
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; VOLUME:
; PAGES:
; DATE: 1
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LOCATION: 1..278
IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
OTHER INFORMATION: /sta
PUBLICATION INFORMATION:
AUTHORS: Weber, J. L.
                                                                                                                                                                                                                                                                                                        DATE: 1
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NAME/KEY:
LOCATION:
IDENTIFIC
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LOCATION:
OTHER INFO
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AUTHORS:
AUTHORS:
TITLE:
TITLE:
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LOCATION: complement (198..217)
IDENTIFICATION METHOD: experime
OTHER INFORMATION: /evidence= E:
OTHER INFORMATION: /standard_name
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                                                                                    TION: 20..39
TIFICATION METHOD:
R INFORMATION: /evi
R INFORMATION: /sta
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TION: 76..118
R INFORMATION: /rpt_:
R INFORMATION: /rpt_:
R INFORMATION: /citat
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S: May, P. E.
S: Kwitek, A. E.
S: Xiao, H.
S: McPherson, J. D.
S: Wasmuth, J. J.
Mapping of human chromosome 5
polymorphisms
L: Genomics
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                                        imilarity 30.5
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NFORMATION: /standard_name= "Onlv -
N INFORMATION:
Weber, J. L.
Polvman
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May, Paula E.
Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
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  /evidence= EXPERIMENTAL
  /standard_name= "PCR primer"
  /citation= ([1])
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/evidence= EXPERIMENTAL
/standard_name= "PCR primer"
/citation= ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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Pred. No. 3.1;
25; Mismatches
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US-08-162-081B-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                 Patent No
GENERAL
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Best Local
                                                                                                                        Sequence
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/323,170B

FILING DATE: 13-OCT-1994

CLASSIFICATION: 424
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APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                          APPLICANT:
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                      TITLE OF INVENTION:
                                                APPLICANT:
CORRESPONDENCE
                                                                                     APPLICANT:
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LENGTH: 9636 base not
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5 OF INVENTION:
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                                                                                                             34, Application US/08162081B
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California
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Bala; Waterfield,
Joseph; Otsu, Masa
                                              Stefano;
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Center, 8
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US-08-162-081B-3
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FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                  GENERAL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                    TITLE OF INVENTION: TH NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
               CURRENT
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COMPUTER READABLE FORM:
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OPERATING
SOFTWARE:
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STATE:
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
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                              SOFTWARE
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INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, INVENTION: THEIR PREPARATION AND USE
SEQUENCES: 50
                                        YPE: Diskette, 5.25
: IBM PS/2
G SYSTEM: PC-DOS
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    IBM PS/2
; SYSTEM: PC-DOS
ION NUMBER:
              : Wordperfect
PLICATION DATA:
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larity 34.2%; Pred. No. 13;
Conservative 20; Mismatches
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4.8%; Score 28; DB 3;
Best Local Similarity 34.2%; Pred. No. 13;
Matches 26; Conservative 20; Mismatches
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2535 GGGACTTATTGAGGTG 2550
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em_hum1:

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PATENT: WO 9849334-A 05-NOV-1998;
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/strain="TYPE A (REV-A)"
/db_xref="taxon:11636"
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Viruses; Retroid viruses; Retroviridae; Mammalian type
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/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE
/db_xref="taxon:11636"
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Portarlington Road, Geelong,
Location/Qualifiers
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/db_xref="taxon:10261"
/note="standard vaccine strain f
Ltd, Castle Hill, New South Wale
ECORI/PstI 4.3kb fragment from t
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integrated reticuloendotheliosis
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FIEISMQRCFSIKSVTDSTVLYIENRTNRYSISTSHDKNEPYEENGIIMNNIECYFVA
CLEGSCTVNVNLGDRQISDNISESSGFLMDVNTDHVIDTKYVGLFITKIKVDAHVFYG
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/note="ORF1"
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integration site; provirus; terminal repeat spleen necrosis virus.

SM Spleen necrosis virus
viruses; Retroid viruses; Retroviridae; Mamm retroviruses; 1-Mammalian type C virus group 1 (bases 2 to 470)
Shimotohno, K., Mizutani, S., and Temin, H.M. sequence of retrovirus provirus resembles the transposable elements provirus resembles the Nature 285 (5766), 550-554 (1980)
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O'Rear, J.J. and Temin, H.M.
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spontaneous changes in nucleotide-sequence in provinuses
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ACRITR1 1005 bp ss-RNA VRL 27
Reticuloendotheliosis virus 713 proviral clone RNA.
M22223 M10659 M16722
M22223.1 GI:209708
long terminal repeat (LTR).
Reticuloendotheliosis virus (from chicken line 151-5 cDNA to mRNA, clone 713.
M Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian ty retroviruses; 3-Reticuloendotheliosis virus group.
1 (bases 99 to 195)
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J. Virol. 54, 161-170 (1985)

E 85135063

E (bases 1 to 1005)

S Swift,R.A., Boerkoel,C.F., Ridgway,A., Fujita,D.J., Dodgson,J.B. and Kung,H.-J.

B-lymphoma induction by reticuloendotheliosis virus: Characterization of a mutated chicken syncytial virus provirus involved in c-myc activation

J. Virol. 61, 2084-2090 (1987)
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1 (bases 1 to 545)

Filardo, E. J., Lee, M.F. and Humphries, E.H.

Structural genes, not the LTRs, are the primary determinants of reticuloendotheliosis virus A-induced runting and bursal atrophy Virology 202 (1), 116-128 (1994)

94279132

GenBank staff at the National Library of Medicine created this
                                                                                                                                                                         Reticuloendotheliosis virus A.
Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae;
retroviruses; 3-Reticuloendotheliosis v.
1 (bases 1 to 545)
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            133
                                                     INCBI gibbsq 148190] from the original journal article. sequence comes from Fig. 3.

Location/Qualifiers
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Gallid herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
1 (bases 1 to 585)
1 (bases 1 to 585)
Jones,D., Brunovskis,P., Witter,R. and Kung,H.J.
Retroviral insertional activation in a herpesvirus: transcriptional activation of U(S) genes by an integrated long terminal repeat in a Marek's disease virus clone
J. Virol. 70 (4), 2460-2467 (1996)
96183893
                                                                                                                                                                                                                                                           inclusive strain CSV
                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created entry [NCBI gibbsq 178131] from the original journal artic This sequence comes from Fig. 1C.
Authors indicate intervening sequence from nt 23 to nt 559 inclusive derived from co-infecting reticuloendotheliosis
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Pred. No. 2.2e-36;
52; Mismatches 11;
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virus insertion.

SM Gallid herpesvirus 2

Viruses; dsDNA viruses, no RNA stage; Herpesviridae.

Yiruses; dsDNA viruses, no RNA stage; Herpesviridae.

This sequence, comes, no RNA stage; Herpesvirus and Kung, H.J.

Retrovirus insertion into herpesvirus in vitro and in vivo Retrovirus insertion into herpesvirus in vitro and in vivo Retrovirus and Retrovirus and
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                                                           ACRLTR2 887 bp ss-RNA VRL 27-APR-1993
ON Reticuloendotheliosis virus 713 proviral clone RNA.

N M22224 M10660 M16722
N M22224.1 GI:209709
long terminal repeat (LTR).
Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas),
cDNA to mRNA, clone 713.
SM Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian type C
retroviruses; 3-Reticuloendotheliosis virus group.

E 1 (bases 510 to 602)
S Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J.
Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J.
c-myc activation in chicken B lymphomas: Detection and mapping of two RNA initiation sites within the reticuloendotheliosis virus
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larity 62.4%;
Conservative 55
                         terminal repeat
.rol. 54, 161-170 (1985)
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/insertion_seq=""
/db_xref="taxon:10390"
145 c 123 g 149 t
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Pred. No. 2.3e-35;
5; Mismatches 15;
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1 JM-Hi3,
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Spleen necrosis virus
Viruses; Retroid viruses; Retroviri
retroviruses; 1-Mammalian type C vi
1 (bases 1 to 859)
Shimotohno, K., Mizutani, S. and Temi
Sequence of retrovirus provirus res
transposable elements
Nature 285 (5766), 550-554 (1980)
80254544
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Swift,R.A., Boerkoel,C.F., Ridgway,A., 1
and Kung,H.-J.
B-lymphoma induction by reticuloendothel
Characterization of a mutated chicken sy
involved in c-myc activation
J. Virol. 61, 2084-2090 (1987)
87226389
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necrosis virus
5 J02389
5.1 GI:61794
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/note="cellular DNA"
/organism="Spleen necrosis v
/db_xref="taxon:11836"
a 199 c 214 g 201 t
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/note="cryptic intron :
a 216 c 227 g :
0 bp after segment 1.
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/proviral
/db_xref="taxon:11836"
741. .>859
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/db_xref="taxon:11836"
<1. .740</pre>
                                                                                                                                                                                      Location/Qualifiers
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/db_xref="taxon:11636"
246. .750
/note="3' LTR"
805. .806
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Pred. No. 1.9e-34;
53; Mismatches 10;
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 Score 121; DB Pred. No. 1e-28; Mismatches
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type C virus
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Spleen necrosis virus proviral DNA/chicken DNA (clone 70), 3'
junction.

N M12248

M12248.1 GI:212691
integration site; proviral gene.
2 of 2
Chicken DNA and proviral spleen necrosis virus DNA.
Chicken DNA and proviral spleen necrosis virus DNA.

SM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
Shimotohno, K. and Temin, H.M.
Evolution of retroviruses from cellular movable genetic elements
Cold Spring Harb. Symp. Quant. Biol. 45, 719-730 (1981)
                                                                                                                                                                                                                    cggacu
|||||:
SNVLTR 180 bp DNA V
spleen necrosis virus LTR.
X59450
X59450.1 GI:61992
LTR.
Spleen necrosis virus.
Spleen necrosis virus
Viruses; Retroid viruses; Retroviridae; M
retroviruses; 1-Mammalian type C virus gr
1 (bases 1 to 180)
Iwasaki,K. and Temin,H.M.
The efficiency of RNA 3'-end formation is distance between the cap site and the pol necrosis virus
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TGAATCCGTAGTACTTCGGTACAACATTT 152
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/db_xref="taxon:9031"
_31 c 47 g 47
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                                                        Retroviridae;
type C virus
        poly(A) site in spleen
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Spleen necrosis virus proviral DNA/chicken
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integration site; proviral gene.
2 of 2
Chicken DNA and proviral spleen necrosis vi
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1 (bases 1 to 160)
Shimotohno, K. and Temin, H.M.
Evolution of retroviruses from c
Cold Spring Harb. Symp. Quant. B
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Pred. No. 7.2e-23;
42; Mismatches 14;
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Aves; Neogi
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46.1 GI:212688
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Yota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                     en DNA and proviral spleen necrosis virus DNA.
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/db_xref="taxon:9031"
34 a 34 c 46 g 46 t
4.5 kb downstream of segment 1
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Search time 205.61 Seconds (without alignments) 703.327 Million cell updates/sec

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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157 27.2 536 X261109 Phaseolus Luw aur ## 157 26.9 1812 X18925 Heat-resistant bar ## 157 26.9 1812 X18925 Heat-resistant bar ## 158 2.7 1812 Y74552 Heat-resistant bar ## 162570 Heat-resistant bar ## 1762572 Heat-resistant bar ## 176257
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Query Match Best Local Similarity 100.0%; Matches 578; Conservative 0

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RW 25 Sequence derived from the 5' end of REV-A;

RW 27 Sequence derived from the 5' end of REV-A;

RW 27 Sequence derived from the 5' end of REV-A;

RW 27 Sequence derived from the 5' end of REV-A;

SY Reticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;

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           72.2%;
64.0%;
ative 10
                             160;
                            Score 417.4;
Pred. No. 3.5e
0; Mismatches
                                 5e-
                                    BB
                            )В 1;
·126;
·31;
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                                   Length
                            Indels
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                                    3878;
                            22;
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RESULT
Q76040
ID Q7
          Query Matc
Best Local
Matches 3
                                                                   We cytomegalovirus; cMV; intermediate-early promoter; IE promoter; We cytomegalovirus; cMV; intermediate-early promoter; IE promoter; We gene therapy; ss.
Spleen necrosis virus.
No9429437-A.
Decripy4.
Pro-JUN-1994; U06415.
Pro-JUN-1994; U06415.
Pro-JUN-1993; US-073345.
Pro-JUN-1994; Univ NEW JERSEY.
Dornburg RC;
Pro-JUN-1993; US-073345.
Pro-JUN-1994; US-073345.
Pro-JUN
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Q76040;
20-JUL-1995
Retrovirus v
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vector; pPO111-R3; spleen necrosis virus; SNV;
virus; CMV; intermediate-early promoter; IE promoter;
nal repeat; LTR; encapsidation; gene transfer;
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    70.9%;
62.9%;
Score 410; DB 1;
Pred. No. 1.1e-123;
61; Mismatches 30;
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                               Length 5519;
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Indels

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Gaps

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Conservative

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RESULT

O76039
O76039 standard; DNA; 5525 BP.

ID Q76039;
AC Q76039;
Tectrovirus; vector pp0111-R2; spleen necrosis virus; SNV;
RW Retrovirus vector; pp0111-R2; spleen necrosis virus; SNV;
RW Retrovirus; vector; pp0111-R2; spleen necrosis virus; SNV;
RW Retrovirus; CMV; intermediate-early promoter; IE promoter;
RW long terminal repeat; LTR; encapsidation; gene transfer;
RW long terminal repeat; LTR; encapsidation; gene transfer;
RW gene therapy; SS
Spleen necrosis virus.
PN W094.29437-A.
PD 22-DEC-1994; U06415.
PN W094.29437-A.
PD 22-DEC-1994; U06415.
PN W094.29437-A.
PD 22-DEC-1994; U06415.
PN W094.29437-A.
PN W094.2944-A.
PN W04.2944-A.
PN W04.2944-A.
PN W04.2944-A.
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RESULT 7
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Q76038;
AC Q76038;
DT Q76038;
DE Retrovirus v
KW Retrovirus;
KW cytomegalovi
KW cytomegalovi
KW long termina
KW long termina
KW long termina
KW 22-DEC-1994;
PD 22-DEC-1994;
PF 07-JUN-1993;
PA (UYNE-) UNIV
PI Dornburg RC;
DR WPI; 95-0364
PT Recombinant
PT ability to p
PT host cell an
PS Example; Pag
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Matches
                                              long terminal represent therapy; ss. spleen necrosis vw09429437-A. 22-DEC-1994. U06407-JUN-1993; US-0(UYNE-) UNIV NEW
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WPI; 95-0364
Recombinant
ability to p
host cell an
Example; Pag
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imilarity 62.9%;
; Conservative 161
  nt retrovirus vector, contg.
produce progeny virus, in
and form provirus
age 13-14; 28pp; English.
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vector pPO111-R1.
vector; pPO111-R1; spleen necrosis virus; SNV;
virus; CMV; intermediate-early promoter; IE promoter;
nal repeat; LTR; encapsidation; gene transfer;
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                                  467/05.
                                                U06415.
US-073345.
NEW JERSEY.
                                                                                       virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s; Score 410; DB 1;
s; Pred. No. 1.1e-12
161; Mismatches 3
                                                                                                                                                    ВP
                    . non-retroviral gene, helper cell which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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Query Match
Best Local Similarity 62.9%; pred. No. 1.16
Matches 381; Conservative 161; Mismatches
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Sequence 5528 BP; 1265 A;
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20-MAY-1999 (first entry)
FOWLPOX virus (FPV M5) LTR sequence.
FOWLPOX virus; FPV; recombinant; reticuloendotheliosis virus chicken; LTR; long terminal repeat; ss.
FOWLPOX virus.
FOWLPOX virus.
18-FEB-1999.
18-FEB-1999.
19-AUG-1998; AU-008454.
POR-AUG-1997; AU-008454.
R (CSIR ) COMMONWEALTH SCI & IND RES ORG.
R (CSIR ) COMMONWEALTH SCI & IND RES ORG.
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X26110;
X26110;
20-MAY-1999
FOW1POY
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es 30;
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Boyle DB, Coupar BEH, Gould AR, Hertig C;

PR WPI; 99-167428/14.

PR Recombinant vaccine against fowlpox virus is free of contamination procure of chickens are combinant fowlpox virus (FPV) whose nucleic from reticuloendotheliosis virus, used to prevent the virus procured in chickens are recombinant fowlpox virus (FPV), and occurrence in relates to a recombinant fowlpox virus (FPV), and procure of solution and the incidence. The vaccine is used to produce an active reticuloendotheliosis virus (FPV), and cald does not encode an active reticuloendotheliosis virus (FPV), and those genome does not contain any REV sequence. The vaccine is used to produce a vaccine against fowlpox virus in chickens. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The vaccine than 1 day of age. Alternatively, chickens can be considered to produce at older than 1 day of age. Alternatively, chickens carry a vaccinated with the vaccine subsequent to vaccine and field strains of any can be prior vaccine and field strains carry a vaccinated be vaccinated with the vaccine strate to infectious REV and (FPV MI) length provirus of REV, and can give rise to infected. The combination provides the means by which a FPV vaccine free from the provice of the provice active free from the number of the provice active present invention provides the means by which a FPV nucleic active present invention by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV may be produced. Sequence selected from the above.

CC contamination of the FPV may be p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γΩ
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Matches 118
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XD XX
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DT C)
26109

X26109;

X2610
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ccurrence in chickens

Example 4; Fig 5; 127pp; English.

Example 4; Fig 5; 127pp; English.

The invention relates to a recombinant fowlpox virus (FPV) whose nucleic reacid does not encode an active reticuloendotheliosis virus (REV), and cald does not encode an active reticuloendotheliosis virus (REV), and cald does not encode any REV sequence. The recombinant FPV is recided to produce a vaccine against fowlpox virus. The vaccine is used to used to produce a vaccine against fowlpox virus in chickens. The chickens can be compared than 1 day of age. Alternatively, chickens older than compared at older than 1 day of age. Alternatively, chickens older than compared than 1 day of age. Prior vaccine and field strains of the vaccine and field strains of the representation with the vaccine of the representations of the representations. The representation provides the means by which a FPV vaccine free from transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from the present invention provides the means by which a FPV vaccine free from the present invention provides the means by which a FPV vaccine free from the present invention provides the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the means by which a FPV vaccine free from the province of the province of
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66.7%; Pred. No. 1.1e-41;
Live 53; Mismatches 5;
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contamination |
Sequence 512

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W09904004-A1. 28-JAN-1999 15-JUL-1998; U14904 18-JUL-1997; US-897175. (DUPO) DU PONT DE NEMOURS &

RESULT X18925

456

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397

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В

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В

373

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Query Match Best Local Matches

PR (HUMA') HUMAN USER.

PI Harash SC, Choi GH, Dillon FL,

PI Rosen CA,

PT Polyvected SC, Choi GH, Dillon FL,

PT Polyvected on computer readable medium and used in the production of anti-S.aureus vaccines medium and used in the production of the invention. The DNA sequences of Stabnylococcus aureus of the invention. The DNA sequences are recorded on a computer readable commonly (RNA), read-only memory (RNA), or CD-RNA. Homology searches using the used in a vaccine composition sputative functions to be assigned so pypeptides can also be used in a vaccine composition spatial st. Specifically, required so pypeptides can also be used in a sample. S.aureus is implicated and these polypeptides can expical wound infections, scalafed of kind these polypeptides can expical wound infections, scalafed skin sinfection in the composition of the polypeptides. The new DNA sequences of any of the S.aureus DNA sequences can be used in the Saureus DNA seque RESULT 11

V74552

ID V74552;

TO V74562;

TO V74562; "these bases represent a line of missing text the sequence listing in the specification. The are included to maintain the nucleotide number given in the specification for this DNA seque "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" "these bases represent a line of missing text in the sequence listing in the specification. They given in the specification the nucleotide numbering 2880 Indels Ô Gaps numbering Ó They

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ESUL.
(62572).

ID T62572.

AC T62572;

DT 27-CCT-1997 (-
DE Heat-resistant ba.

KW Barley; heat resistan.

KW Plant; improved maturativ.

OS Hordeum vulgare.

PN W09702353-A1.

PD 23-VAN-1997.

PF 05-JUL-1996; J01866.

PA (SAPB) SAPPORO REWERIES.

PI ICO K, Kihara M, Okada Y, Yoshigi N;

PT Expression promoter for genes inserted into plant seeds heat-resistant beta-amylase gene inserted into barley seeds

Example 6; Page 20-21; 33pp; Japanese.

CC from a barley beta-amylase (EC 3.2.1.2) gene and other sequences used for integration of this promoter into a reporter plasmid. The seed for the production of transgenic barley plants

Such plants and seeds have improved maturation properties

AB 2 C; 395 G; 614 T;
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T62570
ID
T62570
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762570 standard; DNA; 1276 BP.
762570;
762570;
27-OCT-1997 (first entry)
Heat-resistant barley beta-amylase gene promote Barley; heat resistant; promoter; genetic engineration; ds.
Hordeum vulgare.
W09702353-A1.
05-JUL-1996; J01866.
05-JUL-1995; JP-191028.
(SAPB ) SAPPORO BREWERIES.
Ito K, Kihara M, Okada Y, Yoshigi N;
WPI; 97-108966/10.
Expression promoter for genes inserted into place plant of the promoter defineration promoter is used for the claim 5; Page 17-18; 33pp; Japanese.
762570 is a heat resistant promoter derived from transgenic barley plants and seeds. Such plant; improved maturation properties.
Sequence 1276 BP; 393 A; 237 C; 234
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27.1%;
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Pred. No. 2.6
B; Mismatches
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genetic engineering;
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plants a
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Best Loo
Matches
                       EP-173552-A.
05-MAR-1986.
23-AUG-1984; US-644
06-NOV-1984; US-668
26-JUL-1985; US-758
(UPJO) UPJOHN CO.
Goodwin EC, Palermo
Woychik RP;
WPI; 86-063386/10.
N-PSDB; N60157.
New recombinant DNA
cells - contg. poly
selection marker
Disclosure; Page 5;
This cattle growth
     expression
Sequence
                   This cattle recombinant
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N60157;
04-AUG-1991 (
Cattle growth |
Somatotropin; (
ss.
Bos taurus.
Key
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GTTTCCTTAATTTATTTCATGCCTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTAATGTTCAAACGTGTCCACTAGAGTTCAAGTCTCAGACTTGACATTTGTGTTTGCAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
23
Page 5; 32pp; English.
growth hormone sequence is part of
DNA which is especially useful for
of tissue plasminogen-activator.
2205 BP; 432 A; 616 C; 702
                                     nant DNA for polypeptide expression tg. poly:adenylation signal, coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   imilarity 27.:
; Conservative
                                                                                        Palermo DP,
                                                                                                        306017.
US-644306.
US-668764.
US-758517.
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hormone (somatotropin)
growth hormone; tissue
                                                                                                                                                                                              /number- 4
1480. .1753
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                                                                                                                                                     /number= 4
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                                                                                                                       EP-112012-A.

D 27-JUN-1984.

D 27-JUN-1983; 306655.

F 01-NOV-1983; 306655.

F 01-NOV-1982; US-439683.

R 08-NOV-1982; US-439683.

R (UYCA-) CASE WESTERN UNIV.

I Rottmann FM, Woychik RP, Nilson JH;

R P-PSDB; P40104.

C Claim 1; Page 10-12; 15pp; English.

C Genomic clones p lamda GH2R-2 and -3 are new. They are deposited genomic clones p lamda GH2R-2 and B-15154 and B-15155 resp. The cylin B-101 as host as NRRL B-15154 and B-15155 transformants can be condiced the synthesis of BGH in a eucaryotic host.

C Sequence 2205 BP; 434 A; 614 C; 702 G; 452 T;
                                   Query Match 5.3%;
Best Local Similarity 43.2%;
Matches 54; Conservative
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sequence of genomic bovine
Growth promoter; hormone;
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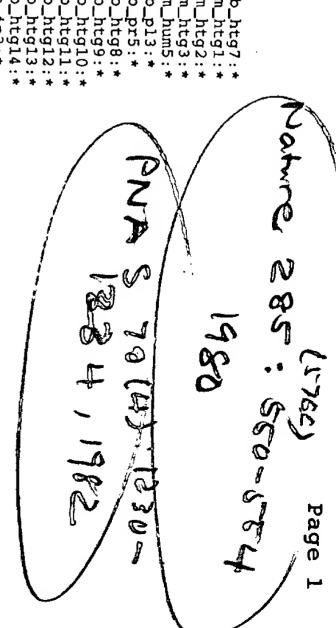
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Gabus-Darlix,C. and Darlix,J.
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Patent: WO 9849334-A 05-NOV-1998;
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retroviruses; 3-Reticuloendotheliosis virus group
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/organism="Reticuloendotheliosis virus"
/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE
/db_xref="taxon:11636"
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/gene="gag"
/gene="gag"
/codon_start=1
/product="gag"
/product="pro/pol"
/product="pro/pol"
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/strain="S (standard vaccine strain)"
/db_xref="taxon:10261"
/note="standard vaccine strain from C
Ltd, Castle Hill, New South Wales, Au
EcoRI/PstI 4.3kb fragment from the 9.
fragment
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/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="AAC58238.1"
/db_xref="GI:2393893"
/translation="MATVARMYKTINTTGISCVLKSLIPDSYNEEYNIDDLDLLKIKE
FIEISMQRCFSIKSVTDSTVLYIENRTNRYSISTSHDKNEPYEENGIIMNNIECYFVA
CLEGSCTVNVNLGDRQISDNISESSGFLMDVNTDHVIDTKYVGLFITKIKVDAHVFYG
QNVIMFPEKNLFSQTNGPNFILYDITVQDRNVLLLITSKYIYNLCDDKYYDIFELKYL
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N V01200 J02387

V01200.1 GI:61757

integration site; provirus; terminal repeat.
Spleen necrosis virus.

Syleen necrosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 1-Mammalian type C virus group.

S Shimotohno, K., Mizutani, S. and Temin, H.M.
Sequence of retrovirus provirus resembles that of
Nature 285 (5766), 550-554 (1980)

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Spontaneous changes in nucleotide sequence necrosis virus, an avian retrovirus
Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-82174569
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GCKPHRTSKVLLASQKVNPRRPVLPSAPESPPRIRRAQFLDERPLSPAPAPAPPPPYPEV
SAIVEDTREGQQPDSTVMTSPPHTRSGLEFGAQGPSGMYPLRETGERDMTGRPMRTYV
SAIVEDTREGQQPDSTVMTSPPHTRSGLEFGAQGPSGMYPLRETGERDMTGRPMRTYV
VRTESRREVRNDQGVQVTDEREIEAQFPATRPDWVGS"
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M Spleen necrosis virus

Viruses; Retroid viruses; Retroviridae; Mammalian

viruses; Retroid viruses; Retroviridae; Mammalian

retroviruses; 1-Mammalian type C virus group.

1 (bases 1 to 891)

1 (bases 1 to 891)

Shimotohno, K., Mizutani, S. and Temin, H.M.

sequence of retrovirus provirus resembles that of

transposable elements

Nature 285 (5766), 550-554 (1980)

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Rattus norvegicus, OTSUKA clone, OT29.32/731c09, microsatellite
sequence, sequence tagged site.
AU025522
AU025522.1 GI:4515445
STS.
Rattus norvegicus DNA, clone:OT29.32/731c09.
Rattus norvegicus ENA, clone:OT29.32/731c09.
Rattus norvegicus Enaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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,K., Okuno,S., Ono,T., Tsuji,A., Hayashi,H., Adachi,M.,
asaki,Y., Iriye,Y., Takahashi,E., Takagi,T., Nakamura,Y. and
igami,A.
  large-scale mapping of ublished (1998) (bases 1 to 290)
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/db_xref="taxon:11836"
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/organism="Gallus sp."
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/db_xref="taxon:9036"
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/organism="Spleen necrosis virus"
/db_xref="taxon:11836"
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'db_xref="taxon:9036"

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55; Mismatches 11;
                               rat microsatellite
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                                                                                                                                     Watanabe, T.K.

Direct Submission
Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi
Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi
K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GEN Research
Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima
771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp,
Tel:81-886-65-2888, Fax:81-886-37-1035)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence,
AU026236
AU026236.1
STS.
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Rattus no
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Direct Submission
Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank datal K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GI Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, 771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp, Tel:81-886-65-2888, Fax:81-886-37-1035)

Location/Qualifiers
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/db_xref="taxon:10116"
/clone="0T29.32/731c09"
/note="0T29.32/731c09F=5'-GATTAGGGGACAAGGGGCT-3'
0T29.32/731c09R=5'-TCTGATATTCATACATGGGCTGC-3'"
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N Homo sapiens ...
SEQUENCE, 14 unorder.

N AC020935

S HTG; HTGS_PHASE1; HTGS_DRAFT.

human.

HOmo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mar
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 113440)
DOE Joint Genome Institute.
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Center Code: JGI
Web site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 106221 bases at least Q40
Consensus quality: 108221 bases at least Q20
Consensus quality: 108903 bases at least Q20
Consensus quality: 108903 bases at least Q20
Estimated insert size: 113440; sum-of-contigs estimation
Estimated insert size: 115000; pulse field gel estimation
Quality coverage: 6.27x in Q20 bases; pulse field gel estimation
Quality coverage: 6.35x in Q20 bases; sum-of-contigs estimation
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2 (bases 1 to 113440)

DOE Joint Genome Institute.

Direct Submission

Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Submitted (12-JAN-2000) Production Sequence (12-JAN-2000) Production Facility Production Facil
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Direct Submission
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MO 63108, USA
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On Apr 28, 1999 this sequence version replaced gi:4337282.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping sequencing collaboration between the NHGRI Chromosome 7 Mapping sequencing certor), John D. McPherson in the Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send

FEATURES

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The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-1161G23, 200 bp overlap. Actual start of this clone is at base position 83123 of RP5-1161G23; actual end is at 70480 of RP5-909F12.

Location/Qualifiers

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/clone="RP5-909F12"
/clone=lib="RPCI-5"
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Ly="MER4-0
                                                                                          Score 37; DB Pred. No. 1.2; 31; Mismatches
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Homo sapiens chromosome UL clc
SEQUENCE, 18 unordered pieces.
AC019045
AC019045.4 GI:7230851
HTG; HTGS_PHASE1; HTGS_DRAFT.
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MO 63108, USA
On Mar 13, 200
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Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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contig of 1455 l
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contig of 2700 l
gap of unknown
contig of 2947 l
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contig of 2739 l
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contig of 6344 l
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contig of 5189 l
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contig of 5817 l
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Mouse enzyme E1 (E1) pseudogene, compl
M88481

M88481.1 GI:193034

enzyme E1; pseudogene.

Mus musculus (strain 163H) male DNA.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata
Eutheria; Rodentia; Sciurognathi; Muri
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1. Genome (1992) In
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45870: contig of 6405 bp in len
871
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971
54439: contig of 8469 bp in len
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63883: contig of 9344 bp in len
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63983: gap of unknown length
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73653: contig of 9670 bp in len
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73753: gap of unknown length
83830: contig of 10077 bp in len
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99389: contig of 15459 bp in len
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152
173618: contig of 34467 bp in len
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Contig of 34467 bp in len
16063
1. 173618
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Submitted (16-NOV-1999) Celera Genomics, 45 West G
Rockville, MD, USA
This sequence was identified as CDM:10211489 by th
For further information on this sequence e-mail to
* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
* by the finished sequence as soon as it is availa
* the accession number will be preserved.
Location/Qualifiers
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AC014255
AC014255.1 GI:6437080
HTG; HTGS_PHASE2.
fruit fly.
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1 (bases 1 to 16832)
Adams, M. and Venter, J.C.
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Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Burack, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, J.H., Goverara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucler, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Quiles, M., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Direct Submission

L. Unpublished

2 (bases 1 to 2007)
                                                                                                                                                                                                            Worley, K.C.

Direct Submission

L Submitted (18-SEP-1999) Human Genome Sequencing Center, Departme of Molecular and Human Genetics, Baylor College of Medicine, One Medicine, Plaza, Houston, TX 77030, USA

On Sep 22, 1999 this sequence version replaced gi:5902995.

* NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces are is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as as as soon as it is available and the accession number will
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RS Glile, R. 1614958)

Butenhoff, C. Champe, M. Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Calle, R., George, R.A., Harris, N.L., Hoskins, R.A., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Moshrefi, M., Nixon, R., Pacleb, J.M., Park, S., Pfeiffer, B., Sequencing of Drosophila melanogaster

BL Unpublished

2 (bases 1 to 114958)

CE Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Celniker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Doyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Buyel, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Farfan, D. E., Galle, R., George, R.A., Harris, N.L., Boyle, C. M., Sarra, K., Kaarney, L., Land, R., George, R.A., Harris, N.L., Boyle, R., George, R.A., Harris, N.L., Bracker, S., Land, R., Sarra, R., Sarra, R., Sarra, R., Sarra, R., Sarra, R., Sarra, R., 
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Drosophila melanogaster chromosome 3 clone BACR43K14 (D968) RPCI-98
43.K.14 map 85D-85D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
***, 88 unordered pieces.
AC008356
AC008356.3 GI:6978383
HTG; HTGS_PHASE1.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Search completed: August 7, 2000, 10:55:16 Job time: 6090 sec

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  RESULT 1

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Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLCY & Lardner
STREET: 1800 Diagonal Road, Suite 500
STATE: VA
COUNTRY: USA
COUNTRY: US
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US-07-800-364B-13
US-07-989-847-11
RE34606-4
US-08-322-965-1
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Sequence 1, Application US/08793599; Patent No. 5952489; GENERAL INFORMATION:
APPLICANT: OKADA, YUKIO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: ITO, KAZUTOSHI
APPLICANT: KIHARA, MAKOTO
TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
FILE REFERENCE: 2589-0056-0 PCT
CURRENT APPLICATION NUMBER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER APPLICATION NUMBER: JP 191028/1995
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 3
NUMBER OF SEQ ID NOS: 3
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                   RESULT 3
US-08-793-599-3/c
US-08-793-599-3/c
; sequence 3, Application U
; patent No. 5952489
; GENERAL INFORMATION:
; APPLICANT: OKADA, YUKIO
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Best I
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Best Local Similarity 27.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Barley 08-793-599-1
                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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APPLICANT:
           APPLICANT:
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                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                  GTTTCCTTAATTTATTTCATGCCTT
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| Similarity 4.5%;
| 13; Conservative 1
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YOSHIGI, NAOHIRO
ITO, KAZUTOSHI
                        YUKIO
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pred. No. 0.0073;
156; Mismatches 117;
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                                                                                                                                                                                                                 Score 30.6; DB pred. No. 0.67; Nismatches
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; LENGTH: 21
; TYPE: DNA
; ORGANISM:
US-08-793-599-
                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: I
; OTHER INFORMATION: S
US-09-226-568-18
RESULT 5
US-08-077-848A-1/c
; Sequence 1, Application
; Patent No. 5470955
; GENERAL INFORMATION:
; APPLICANT: Craig, Resident of invention:
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Best Local S
Matches 23
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 18
LENGTH: 3934
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No
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                                                                                                                                                                                    Matches
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Best Local
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APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
FILE REFERENCE: ISPH-0337
                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ISPH-0337

CURRENT APPLICATION NUMBER: US/09/226,568

CURRENT FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 39
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18, Application US/09226568
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27; Conservative
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Conservative
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LOCATION: 61..1110

COTHER INFORMATION: 61..1110
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JS-09-211-640-1/c
Sequence 1, Application US/09211640
Patent No. 6020466
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WH:
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & STREET: 1880 Century Park East,
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VE
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 27
                               COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
IMMEDIATE SOURCE:
CLONE: mc1-1
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STREET: 1880 Century Park
CITY: Los Angeles
STATE: California
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ADDRESS:

ET: 1880 Century Park E:

Los Angeles
3: California

RY: USA
90067
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. Similarity 56.2%;
27; Conservative
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16-JUN-1993
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STREET: 1880 Century Park East, Sui CITY: Los Angeles STATE: California COUNTRY: USA ZIP: 90067

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/03547 FILING DATE: 31-MAR-1994 CLASSIFICATION: NAME: Wetherell, Jr., Ph.D., John FREGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: 51,678 REFERENCE/DOCKET NUMBER: FD-2845 TELEPHONE: (619) 455-5100 TELEPAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 1:
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Best Loc
Matches
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mcl-1
FEATURE:
NAME/KEY: CDS
LOCATION: 61.1110
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9403547
Sequence 1, Application PC/TUS9403547
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE
TITLE OF INVENTION: MCL-1
NUMBER OF SEQUENCES: 2
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ADDRESSEE:
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LOCATION: 61..1110
OTHER INFORMATION: 6
OTHER INFORMATION: 6
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APPLICATION NUMBER:
FILING DATE:
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CLASSIFICATION:
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Similarity 56.2%;
27; Conservative
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TION NUMBER: US
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amino acid 227 = A; when
acid 227 = V."
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Suite 500
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Length 3946;

740 - C, nucleotide

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NAME/KEY: CDS
LOCATION: 61..1110
OTHER INFORMATION: 6
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COTHER INFORMATION: 6
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Matches 2
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                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,945A
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION NUMBER: SE 9300902-5
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
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TOPOLOGY: 11
MOLECULE TYPE:
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APPLICANT:
                                                                                                                                                                                                                                                                                            COUNTRY: United States ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: :
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STATE: New York
       TELECOMMUNI
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Similarity 56.2%;
27; Conservative
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INFORMATION
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Best Local
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ORIGINAL SOURCE:
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                                                  LOCATION: 08-068-945A-1
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LOCATION:
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AX: (212)354-8113
ON FOR SEQ ID NO: 1:
E CHARACTERISTICS:
H: 11531 base pairs
nucleic acid
9.2%;
Similarity 33.6%;
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
join(1722..1727, 4071..4221, 4307..4429, 4707
..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11391)
RMATION: /EC_number= 3.1.1.1
RMATION: /product= "Bile Salt-Stimulated Lipase"
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..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
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   s; Score 28.8; DB
pred. No. 6.9;
24; Mismatches
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8-442-806-1

INFORMATION:

5716817

US/08442806

APPLICANT: Tornell, Jan TITLE OF INVENTION: Gen TITLE OF INVENTION: Enc NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS:

Genomic DNA Encoding Hum

Human

Sequences

Lennart

Peter Gunnar

Jeanette

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NAME/KEY:
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LOCATION:
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LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11391)
OTHER INFORMATION: /EC_number= 3.1.1.1
OTHER INFORMATION: /product= "Bile Salt-Stimulated Lipase"
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51;
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SOURCE:
                                                                                       9.2%; Score 28.8; Dilarity 33.6%; Pred. No. 6.9; Conservative 24; Mismatches
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11491..11531
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10650..11490
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1641..1727
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E: Mammary gland
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..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
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                                                                                   Gaps
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COMPUTER: IBM PC COMPONENTING SYSTEM: PC-1
SOFTWARE: Patentin ReCURRENT APPLICATION DATA

IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,

COMPUTER READABLE MEDIUM TYPE: F)

FORM:

STREET: 1155 AV CITY: New York STATE: New York COUNTRY: United ZIP: 10036-2787

New York

RY: United 10036-2787

States

ADDRESSEE:

Avenue of t

the

Americas

APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-0

APPLICATION NUMBER: FILING DATE: 12-JUN-PRIOR APPLICATION DATA:

יייים אנד SE 9201826-6 12-JUN-1992 טאר איייים אנד

FILING DATE: 11-JUN-PRIOR APPLICATION DATA:

MBER: SE 9201809-2 11-JUN-1992

APPLICATION NUMBER:

LASSIFICATION: 435 OR APPLICATION DATA

APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 27-MAY-1993

08/068,945

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 43

US/08/442,806

Version

TELECOMMUNICATION INFORMATION:

103326-052

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base pairs

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US-08-222-177A-17
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (geno
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIETE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES NUMBER OF SEQUENCES: 460
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ADDRESSEE: DeWitt Ross
STREET: 8000 Excelsior
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COMPUTER READABLE
MEDIUM TYPE: F1
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TISSUE TYPE: BI
IMMEDIATE SOURCE:
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STREET: 80
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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STATE: W
COUNTRY:
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                                                                         NAME/KEY: misc_feature
LOCATION: 72..91
IDENTIFICATION METHOD: 6
OTHER INFORMATION: /evic
OTHER INFORMATION: /star
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OTHER INFORMATION:
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LOCATION: complement (144..163)
IDENTIFICATION METHOD: experimental
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/rpt_family=
/citation= ([
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                                                             D: experimental
/evidence= EXPERIMENTAL
/standard_name= "PCR pr:
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                               Caucasian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17:
                                                                                                                                                                                            "tandem"
/= "(dC-dA)n.(dG-dT)n"
                                                                                                                                                                              ([2])
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                                                                                    "PCR primer"
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; DATE: 198
US-08-222-177A-17
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US-08-222-177A-52
; Sequence 52, Application US/08222177A
; Patent No. 5582979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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AUTHORS:
AUTHORS:
TITLE: Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATE: 1990
PUBLICATION
AUTHORS: 1
AUTHORS: AUTHORS: ADTITLE: ADTITLE: Wh
                                                                                                                            ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..221
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only or
OBLICATION INFORMATION:
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ADDRESSEE
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PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
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                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: May
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INFORMATION:
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S: May, P. E.
Dinucleotide repeat portion of the property of t
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May, Paula E.
Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201-
                                                                                                                                                                                                                                                                                                                                                                                                                            Madison
Wisconsin
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SEQUENCES: 460

SECONDRESS: Stevens, S.C.

8000 Excelsior Drive, Suite 401
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}9
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1..221
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/standard_name= "PCR primer"
/citation= ([1])
                                                                                                                                                                                 US/08/222,177A
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                                                                                                                                                                                                                                            Version
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LOCATION: 20.39
IDENTIFICATION METHOD: e
OTHER INFORMATION: /evide
OTHER INFORMATION: /stance
OTHER INFORMATION: /citate
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IDENTIFICATION METHOD:
OTHER INFORMATION: /evi
OTHER INFORMATION: /sta
PUBLICATION INFORMATION:
AUTHORS: Weber, J. L.
AUTHORS: May, P. E.
AUTHORS: Kwitek, A. E.
AUTHORS: Xiao, H.
AUTHORS: McPherson, J.
AUTHORS: Masmuth, J. J.
TITLE: Mapping of human
TITLE: polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR
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CLONE: Mfd154
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                      PUBLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 278 base pairs
TYPE: nuclei-
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LOCATION: complement (198..2)
IDENTIFICATION METHOD: experi
OTHER INFORMATION: /evidence
OTHER INFORMATION: /standard_
OTHER INFORMATION: /citation
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REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                          AUTHORS:
AUTHORS:
TITLE: P
PAGES: 388-396
DATE: 1989
22-177A-52
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEY:
                                                                                                                                                                                                                                                                            RS: Wasmuth, J. J.

Mapping of human of
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TION: 76..118
INFORMATION:
INFORMATION:
INFORMATION:
                                                                                                                    S: Weber, James L.
S: May, Paula E.
Abundant Class of H
Which Can Be Typed I
Reaction
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Weber, J. L.
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May, P. E.
Kwitek, A. E.
Xiao, H.
                                                                                           A
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1..278
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ISOLATE: Caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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/rpt_family=
/citation= ([
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/evidence= EXPERIMENTAL
/standard_name= "PCR pr.
/citation= ([1])
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/evidence= EXPERIMENTAL
/standard_name= "PCR pr:
/citation= ([1])
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                                                                                                                                                                       Human
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                                                                                                                                         Using
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'- "(dC-c
                                                                                                                                            the
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                                                                                                                                                               Polymorphism
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Chain
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-34
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US-08-162-081
; Sequence 34
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Best Loc
Matches
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CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMB
                                                 2475
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COMPUTER RE
MEDIUM TY
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APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                         200
                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clit
STATE: NC
COUNTRY: US/
COUNTRY: 10022
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                                                                                               26;
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NVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, NVENTION: THEIR PREPARATION AND USE
                                       8.9%; Score 28; DB 2; ilarity 34.2%; Pred. No. 7.2; Conservative 20; Mismatches :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.0%; Score 28.2; Dimilarity 30.5%; Pred. No. 2.1; Conservative 25; Mismatches
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SYSTEM: P
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V York
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N: 435
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                       215
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RESULT 14
US-08-162-081B-32
; Sequence 32, Applicatic
; Patent No. 5824492
; Patent No. 5824492
Hiles,
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; TYPE: nucleic
; STRANDEDNESS:
; TOPOLOGY: lin
US-08-780-872-34
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Matches
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                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13 APTIL 1770
FILING DATE: 13 APTIL 1770
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATRICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 838-38
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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APPLIGATION NUMBER: 08
FILING DATE: February
APPLICATION NUMBER: PO
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805
CITY: New Y
STATE: New
COUNTRY: US
ZIP: 10022
                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PS/2
OPERATING SYSTEM:
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Local Similarity 34.2%;
les 26; Conservative
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: New York
RY: USA
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5824492
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   INVENTION:
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Bala; Waterfield, Michael Derek; Parker
Joseph; Otsu, Masayuki; Panayotou, Georg
Stefano; Gout, Ivan Tarasovitch
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(212) 838-3884
                Stefano;
                             Joseph;
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09-JAN-1997
ON: 435
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יs, Ian Donald; Fry, אבייי
יs, Waterfield, Michael Derek;
eph; Otsu, Masayuki; Panayotou
fano; Gout, Ivan Tarasovitch
fano; Gout, Ivan Tarasovitch
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RESULT 15
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REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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Best I
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                    GENERAL INFOR APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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PRIOR APPLICATION DATA:
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                                                                                                                                                         APPLICANT:
                                                            NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                           APPLICANT:
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                                                                                                                   TITLE OF
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LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
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                       COUNTRY:
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                                                                                               INFORMATION:
INFORMATION:
CANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
CANT: Bala; Waterfield, Michael Derek; Parker, Peter
CANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
CANT: Stefano; Gout, Ivan Tarasovitch
OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
OF INVENTION: THEIR PREPARATION AND USE
R OF SEQUENCES: 50
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SYSTEM: F
EADABLE FORM:
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05 Third Avenue
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                                        York
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February 7, 1994
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Gaps

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MEDIUM TYPE: Diskette, 5.25 inc...,
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 APF11 1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDENNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1.3204
OTHER INFORMATION: /standard_name=
US-08-780-872-32

8.9%: Score 2
34.2%: Pred. N
Search completed: Job time: 908 sec
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        2000,
                                                                                                                                                                   Score 28; DB 3;
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using sw model	GenCore version 4.5 (c) 1993 - 2000 com
	4.5 Compugen Ltd.

Run on: August 2000, 09:21:25 ;

Search time 205.61 Seconds (without alignments) 382.084 Million cell updates/sec

Title: Perfect so Sequence: score: US-09-214-124-2_COPY_265_578
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Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number o H hits satisfying chosen parameters: 623170

Minimum DB Maximum DB seq seq length: 1000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

N_Geneseq_36:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match Best Local Simi Matches 314;

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Score 314; DB 1; Pred. No. 7.4e-91; Mismatches 0;

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17-MAR*1999 (first entry)

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17-MAR*1999 (first entry)

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17-MAR*1999 (first entry)

PT

17-MAR*1999 (first entry)

PT

Sequence derived from the 5' end of REV-A; 5' end genomic RNA;

RR eticuloendotheliosis virus type A; REV-A; 5' end genomic RNA;

RR eticuloendotheliosis virus.

PR

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18-6515-A1

PR

18-APR-1997; D05203.

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18-APR-1997; FR-005203.

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18-APR-1997; FR-005203.

PR

19-30-OCT-1998.

DR

18-APR-1997; FR-005203.

PR

19-30-OST-1998.

DR

19-30-OST-1998.

DR

18-APR-1997; FR-005203.

PR

18-APR-1997; FR-005203.

PR

19-30-OST-1998.

DR

18-APR-1997; FR-005203.

PR

28-APR-1997; FR-005203.

PR

18-APR-1997; FR-005203.

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28-APR-1997; FR-005203.

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18-APR-1997; FR-005203.

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28-APR-1997; FR-005203.

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Best Local Similarity 100.0%;
Matches 314; Conservative
X26113 standard; DNA; 4643 l
X26113;
20-MAY-1999 (first entry)
Fowlpox virus (FPV S) 5' LT!
Fowlpox virus; FPV; recombii
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); Mismatches 0
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995

95 (first entry) s vector pPO115-R1. s; vector; pPO115-R1; sp sfer; gene therapy; ss.

spleen necrosis

rosis virus

U06415. US-073345

tandard; DNA;

3878

ВÞ

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Fowlpox virus.

No Wo9907852-Al.

Fowlpox virus.

No Wo9907852-Al.

PD 18-FEB-1999: AU0628.

PP 08-AUG-1999; AU0628.

PR 08-AUG-1999; AU008454.

PR 08-AUG-1999; AU-008454.

PA (CSIR) COMMONNEALTH SCI & IND RES ORG.

PA (CSIR) COMMONNEALTH S
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Best Loo
Matches
Q76041 stan
Q76041;
Q76041;
20-JUL-1995
Retrovirus;
Retrovirus;
gene transf
Spleen necr
W09429437-A
22-DEC-1994
07-JUN-1993
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Pred. No. 1.9e-87;
93; Mismatches 6;
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RESULT
Q76040
D 076040 standard; DNA; 5519 BP.
C 076040;
C 076040;
P 20-JUL-1995 (first entry)
E Retrovirus vector pp0111-R3;
W Retrovirus vector; pp0111-R3;
W cytomegalovirus; CMV; Intermediate-early promoter; IE promoter;
promo
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Best Local
Matches 1
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R WPI; 95-036467/05.

T Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect thost cell and form provirus

S Example; Page 17; 28pp; English.

C The universal retroviral vector pPO115-R1 (given in Q76041) was cotained by replacing the SV40 promoter and hpt gene of pPO111-R1 (Q76038) with the multiple cloning site of pBluescript II KS. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Q Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T;
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65.8%;
ative (
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; Pred. No. 1e-6
84; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 virus; SNV;
cer; IE promoter;
transfer;
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AC Q76039 s...
AC Q76039;
AC Q76039;
AC Q76039;
DT 20-JUL-1995 (first e...
Extravirus; vector; pp0111-R2; sp...
KW Retrovirus; vector; pp0111-R2; sp...
KW cytomegalovirus; CMV; intermediate-early r
KW dong terminal repeat; LTR; encapsidation; gene ...
Spleen necrosis virus.

May 2-DEC-1994;
PF 07-JUN-1993; US-073345.
PN 009428437-A,
PF 07-JUN-1993; US-073345.
PN 00740N-1993; US-073345.
PN 00740N-1993; US-073345.
PN 00740N-1993; US-073345.
PN 00740-1994; UO6415.
PN 007-JUN-1993; US-073345.
PN 00740-1994; UO6415.
PN 007-JUN-1993; US-073345.
PN 007-JUN-1993; US-073345.
PN 009428437-A,
PF 07-JUN-1993; US-073345.
PN 009428437-A,
PF 07-JUN-1993; US-073345.
PN 009428437-A,
PF 07-JUN-1993; US-073345.
PN 009428437-A,
PF 07-JUN-1994; UO6415.
PN 00942841, UNEXPERIENCE COLUMN CONTROL COLUMN CO
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O76039
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Pred. No. 1.8e-
86; Mismatches
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e-66;
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 γQ
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Retrovirus; vector; pPO111-R1; spleen necrosis virus; SN Retrovirus; vector; pPO111-R1; spleen necrosis virus; SN Cytomegalovirus; CMV; intermediate-early promoter; IE procytomegalovirus; CMV; intermediate-early promoter; IE procytomegalovirus; Sn Spleen necrosis virus.

Spleen necrosis virus.

WO9429437-A.

22-DEC-1994; U06415.

07-JUN-1993; US-073345.

(UYNE-) UNIV NEW JERSEY.

Dornburg RC;
WPI; 95-036467/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and form provirus

Example; Page 13-14; 28pp; English.

Example; Page 13-14; 28pp; English.

New recombination-free, highly efficient retroviral vectors ppoll1-R1 (given in Q76038), ppoll1-R2 (Q76039) and ppoll1-R3 (Q76040) were obtained by replacing the U3 region of the left (Q76040) were obtained by replacing the U3 region of the left and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5528 BP; 1265 A; 1423 C; 1457 G; 1383 T;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.0%;
Best Local Similarity 64.0%;
Matches 208; Conservative
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Q76038;
20-JUL-1995
Retrovirus v
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pred. No. 1.8e
86; Mismatches
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80
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-14;
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infect
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RESULT 8
V74552
ID V74552;
AC V74552;
DT 16-MAR-1999
DE Staphylococcus
KW Computer read
KW cellulitis; es
KW skin infection
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                                                                                              Claim 1; Page 1025-1028; 3271pp; English.

Claim 1; Page 1025-1028; 3271pp; English.

Claim 1; Page 1025-1028; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

Cof the invention. The DNA sequences are recorded on a computer readable

cof the invention. The DNA sequences are recorded on a computer readable

cof the invention. The DNA sequences allows putative functions to be assigned so

cof the saureus DNA sequences allows putative functions to be assigned so

cof that protein-encoding or regulatory regions of commercial, therapeutic or

cof that protein-encode antigens have been identified and these polypeptides can

cof likely to encode antigens have been identified and these polypeptides can

cof likely to encode antigens have been identified and these polypeptides can

cof be used in a vaccine composition against saureus infection. The

cof constant in a sample. Saureus is implicated in numerous human diseases,

cof including cellulitis, eyelid infections, food poisoning, osteomyelitis,

cof syndrome, etc. Organisms transformed with the DNA sequences can be used

cof composition of the polypeptides. The new DNA sequences

cof composition as primers or probes for isolating

cof the composition as primers or probes for isolating

cof the composition as primers or probes for isolating
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30-JUL-1997.
07-JAN-1997;
05-JAN-1996;
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WPI; 97-374922/35.
WPI; 97-374922/35.
Polynucleotide(s) and proteins derived from Staphylococcus aureus Polynucleotide(s) and proteins derived from Staphylococcus aureus Polynucleotide(s) and proteins and used in the production of stored on computer readable medium and used in the production of anti-S.aureus vaccines anti-S.aureus vaccines Claim 1; Page 1025-1028; 3271pp; English.
Claim 1; Page 1025-1028; 3271pp; English.
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997; 100117.
996; US-009861.
HUMAN GENOME SCI INC.
HOMAN GENOME SCI INC.
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                                                             fragments) are useful a of any of the S.aureus eadable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us aureus contig SEQ ID #241.
dable medium; vaccine; S.aureus infection; immunodetection; dable medium; vaccine; S.aureus infection; immunodetection; eyelid infection; food poisoning; osteomyelitis; therapy; on; surgical wound infection; scalded skin syndrome;
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Length 5000;
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T62572 standard; DNA; 2142 BP.
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T62570;
T62570;
27-OCT-1997 (first entry)
Heat-resistant barley beta-amylase generically; heat resistant; promoter; generate; improved maturation; ds.
Hordeum vulgare.
W09702353-A1.
23-JAN-1997.
05-JUL-1996; J01866.
05-JUL-1995; JP-191028.
(SAPB ) SAPPORO BREWERIES.
Ito K, Kihara M, Okada Y, Yoshigi WPI; 97-108966/10.
Frommession promoter for genes insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression promoter for genes inserted into plant heat-resistant beta-amylase gene inserted into ba Claim 5; Page 17-18; 33pp; Japanese.
T62570 is a heat resistant promoter derived from (EC 3.2.1.2) gene. The promoter is used for the ptransgenic barley plants and seeds. Such plants a improved maturation properties.
Sequence 1276 BP; 393 A; 237 C; 234 G;
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Similarity 27.1%;
23; Conservative
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Pred. No. 1.7;
28; Mismatches
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ne inserted into barley s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                 gene promoter containing DNA. genetic engineering; transgenic;
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Best Local
Matches 2
                                                                                                       Zeng Z;
WPI; 99-153691/.
P-PSDB; Y00312.
New isolated hur
useful for diagr
disorders, immur
Claim 1; Page 2;
This sequence re
human protein. I
can be used to g
New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders Claim 1; Page 236-237; 312pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted can be used to generate fusion proteins by linking to the gene to a human the fused protein as compared to the human protein only.

The invention relates to 83 novel genes and their fragments (nucleic acid sequences: X20412-X20499; amino acid sequences y00258-y00377) which are useful for preventing, treating or ameliorating medical conditions
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Carter K
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WO9906423-A1
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secreted protein; fusion protein; gene therapy; protein therapy; sis; tissue; cancer; tumour; neurodegenerative disorder; leukaemi, pmental abnormality; foetal deficiency; blood; allergy; renal; ds system; asthma; lymphocytic disease; brain; hepatic; lymphoma; mation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ive disorder; schizophrenia; prostate; obesity; osteoclast; thymoretine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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US-054217.

US-054218.

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DE Human mcl-1 gene.
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22-DEC-1994: U03547.

31-MAR-1994: U03547.

31-MAR-1993: US-077848.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

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Here myeloid cell leukaemia associated gene mcl-1 - used to new myeloid cell leukaemia associated gene mcl-1 relevelop prods. for detection and treatment of cell prolifer develop prods. for detection and treatment of cell prolifer disorders, partic. myeloid cell leukaemia

T disorders, partic. myeloid cell leukaemia associated gene mcl Disclosure; Page 46-49; 67pp; English.

S Disclosure; Page 46-49; 67pp; English.

C isolated from a cDNA library prepd. from ML-1 human myelok leukemia cells induced with TPA. The predicted gene produced with TPA. The predicted gene produced with TPA. The predicted gene produced with TPA.
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30-NOV-1994; 319525.
30-NOV-1994; JP-319525.
(KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU. WPI; 96-336575/34.
P-PSDB; W03474.
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BSSL/CEL Gen
BSSL; biolog
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larity 25.0%; Pred. No. 14;
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'D 23-DEC-1993.

'P 09-JUN-1992; SE-001809.

'R 11-JUN-1992; SE-001826.

'R 03-JUL-1992; SE-002088.

R 12-JUN-1992; SE-002088.

'R 03-JUL-1993; SE-002008.

'R 12-JUN-1992; SE-000902.

'R 12-JUN-1992; SE-000902.

'R 12-JUN-1992; SE-000902.

'R 12-JUN-1992; SE-002088.

'R 19-MAR-1993; SE-000902.

'A (ASTR ) ASTRA AB.

Bjursell KG, Carlsson PNI, Enerback CSM, Hansson SL;

I Enerback CSM;

R 19-MAR-1993; SE-000902.

'A (ASTR ) ASTRA AB.

Bjursell KG, Carlsson PNI, Enerback CSM, Hansson SL;

I Enerback CSM;

R P-SDB; R45189.

To An encoding bile salt-stimulated lipase/carboxyl ester l substitute, contains intron sequences

Claim 1; Page 43-51; 76pp; English.

C The primers (Q54223-28) are used to amplify fragments of lipase which when expressed by the sanimals can be used as a human milk substitute. The BSSL Can be used as a human milk substitute. The BSSL As it has a broad substrate specificity it can mediate th Sequence lissible salt-stim of sequence lissible salt-stim the small digestion of most dietary lipids.

Sequence lissible salt-stim sequence salt-stim the small digestion of most dietary lipids.
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PD 18-MAR-1999.

PF 08-SEP-1998; U18730.

PF 10-SEP-1997; US-058460.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Sweigard JA;

DR P-PSDB; Y06786.

PT New isolated fungal pathogenicity genes

CC claim 33; Page 47-49; SOpp; English.

CC designated PTH2, PTH3, PTH11 and PTH12 that are obtained from Magnapartha

CC grisea. These novel genes encode proteins (Y06783-86) that are highly

CC imidazole glycerol phosphate dehydratase enzyme, fungal

CC associated pathogenicity protein or fungal homeodomean transcription

CC pathogenicity. Inhibition of any of the genes PTH2, PTH3, PTH11 and PTH12

CC results in the reduction or elimination of the pathogenic phenotype of

CC identify inhibitors of the fungal pathogenic gene products. The solated genes are useful in the design of screens to

CC sequence represents the PTH12 gene sequence.

Query Match

9.18: Screens of the fungal pathogenic gene present

9.18: Screens of the fungal pathogenic gene present
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Query Best I Matche tches 3828 888 121 Local 81 cgucacu 187 |:| |: TGTCTCT 3894 Similarity 22; Conserv 9.1%; Score 28.6; I larity 32.8%; Pred. No. 12; Conservative 21; Mismatches DB 1; 24; Length 4795; Indels <u>.</u> Gaps

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ALIGNMENTS

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B19095 T12K17-Sp6
AA283692 Zt18b01.s
A1963668 wr64e02.x
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AQ785991 HS_3082_B
AQ785991 HS_3082_B
AQ785991 HS_5232_A
AV025658
AA204674 Zr87C08.r
AA305899 EST176897
AW219133 EST301615
AA321452 EST23928
AW628807 h140b04.x
H80010 ys65e11.s1
AA291667 Zt37C12.s
AA883427 am25a12.s
T68051 yC39h11.r1
AA909158 om13e03.s
AL044713 DKFZP434F
AA7148449 ny01d10.s
AA805967 oc20c09.s
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AA765789 oa09g05.s
AA765789 oa09g05.s
AA765789 vr99g10.s
AA749362 nx99g10.s
AA749362 nx99g10.s
AA749362 nx99g10.s
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AA769086 oa74e07.s
AA918504 ol77e01.s
AA7740884 nz03h10.s
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AI664738.1 GI:4775726
EST.
Trypanosoma cruzi
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa; Kinetoplastida; A. and Gonzalez,
Gonzalez Rey,E., Remisz,E., Delgado Garcia,A. and Gonzalez,
Characterization of ESTs from Trypanosoma cruzi epimastigot
Contacterization of ESTs from Trypanosoma cruzi epimastigot
Contacterizat
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GSS.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryol
Magnoliophyta; eudicotyledons; Ro
Brassicaceae; Arabidopsis.
1 (bases 1 to 646)
Feng, J., Dewar, K., Buehler, E., K.
Ecker, J.
BAC End Sequences at ATGC
Unpublished (1997)
Contact: Ecker J.
Arabidopsis Thaliana Genome Centuriversity of Pennsylvania
Dept. of Biology, University of 19104
Tel: 215-898-9384
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nilarity 33.9%;
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/strain="Cl - Brenner"
/db_xref="taxon:5693"
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/note="Site_1: EcoRI; Site_2: NotI; cDNA library
/constructed with oligo dt primed epimastigote mRNA and
constructed with oligo dt primed epimastigote mRNA and
cloned in pt7t318D phagemid with modified polylinker"
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pred. No. 1.8;
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lons; Rosidae; eurosids II;
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                                                                 Pennsylvania,
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Brassicales;
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AI664738 B19095 AA283692 AI963668 AQ785991 AQ785991 AQ556621 AQ0556621 AQ025658 AA204674 AA301452 AW628807 H80010 AA291667 AA883427 T68051 AA909158 AL044713 AA909158 AL044713 AA748449 AA8305967 AA8305967 AA8305967 AA8305967 AA836685 AW1691003 AA749362 AA749362 AA749362 AA749362 AA830151 W31394 AW195146 AN1870684 AW195146 AA1400614 AW152354 AA835787 AA835787 AA287701 AA3769086 AA1962772 AA318504 AA1962772

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E 1 (bases 1 to 296)
S Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags 97044478
E 97044478

Con con 30 1007 + his securons version replaced of 11520551
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              On Sep 29, 1997 this sequence version repla

Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lou
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free throug
Possible reversed clone: similarity on wron
Insert Length: 2216 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 223.

Location/Qualifiers
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Seq primer: Sp6
Class: BAC ends
High quality sequence start: 7
High quality sequence stop: 87
Location/Qualifiers
646
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HindIII; Produced by Rod Wing"
313 c 110 g 155 t 3]
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                                                                                                                                                                                                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D., ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, ph.D.
DNA Sequencing by: Washington University Genome Sec
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1053 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 247.
Location/Qualifiers
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AI963668 AI963668.1 GI:57563(EST. human.
Homo sapiens
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Tumor Gene Index
Unpublished (1997)
On Jul 27, 1999 this sequence version replaced gi:4059330.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tiesine Procurement: Christopher Moskaluk, M.D., Ph.D., Mineral Procurement: Christopher Moskaluk, M.D
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo c
Average insert size 1.75 kb. Life Technologies catalog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Institute, Cancer Genome Anatomy
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/tissue_type="ovarian tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 bp mRNA EST 08-MAR-2000 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492474 contains element MSR1 repetitive element; mRNA
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Primates;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com)
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3082 row: H column: 4
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 371.
Location/Qualifiers
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Similarity 37.3%; Pred. No. 16;
44; Conservative 19; Mismatches
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AQ785991
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Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ785991 371 bp DNA GSS
HS_3082_B2_D02_MR CIT Approved Human Genomic
Homo sapiens genomic clone Plate=3082 Col=4 I
uaauacuuuggagagucuuuugccuccagugucuuccguuuguacucguccuccucuccc
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Mahairas,G.G., Wallace
Keller,A., Shaker,R.,
Hood,L.
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Eutheria; Primates; Catarrhini;
1 to 371)
3.G., Wallace, J.C., Smith, K., Sw
                                                                                                             /note="Organ:
E-Coli DH10B"
a 94 c
                                     23.6%;
ity 37.1%;
servative 19
                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3082 Col=4 Row=H"
/clone_lib="CIT Approved Human Genomic
                                                                                                                                             'sex="male"
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g,J., Zhao,S.,
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Adams,M.D.
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                                                           355
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Contact: Mahairas GG, Wallace JC, Hood L

Contact: Mahairas GG, Wallace JC, Hood L

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Fax: (206) 616-3887

Fax: (206) 616-3887

Clones are derived from the human BAC library RPCI-11. For BAC clones are derived from the human BAC library RPCI-11. For BAC clones are derived from the human BAC library RPCI-11. For BAC pieter@dejong.med.buffalo.edu). Clones may be purchased from (pieter@dejong.med.buffalo.edu). Clones may be purchased from (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
BACPAC Resear h Genetics (info@resgen.com). BAC end Web Server:

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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1 (bases 1 to 487)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
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Hood, L
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993805
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_A2_H02_SP6E RPCI-11 Human Male BAC L.
genomic clone Plate=808 Col=4 Row=0,
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=808 Col=4 Row=0"
/clone_lib="RPCI-11 Human Male BAC Library"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Nector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Nector: pBACe3.6; Site_1: EcoRI; one randomly chosen donor
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
and partially digested with a combination of EcoRI and
ecoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

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pred. No. 20;
[5; Mismatches
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On Jun 15, 1998 this sequence version replaced gi:3222478.
Contact: Chie Owa
                   MANA Sequence.
AA204674
AA204674.1 GIVEST.
  Homo
           human
                                                    AA204674 331 bp
zr87c08.rl NCI_CGAP_GCB1
mRNA sequence.
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Similarity 50.0%;
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Mammalia; Eutheria; )
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sapiens
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                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1200014N20"
/clone_lib="Mus musculus a
/tissue_type="lung"
/dev_stage="adult"
a 68 c 65 g 100
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"T., Sogabe,
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1 (bases 1 to 373)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
                                                                                                                                                        EST.
                                                                                                                                                                           myeloid cell differentiation protein, mRNA sequence AA305899.1 GI:1958>>>
                                                                                                                              Homo sapiens
Eukaryota; M
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Mammalia; Eutheria; F
1 (bases 1 to 331)
NCI-CGAP http://www.n
National Cancer Insti
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strau
Tel: (301) 496-1550
Email: Robert_Straush
This clone is availab
                                                                                                                                                                                                                                                                                                198
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Seq primer: -28M1
High quality sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ill: Robert_Strausberg@nih.gov
Ls clone is available royalty-free through LLNL;
NGE Consortium (info@image.llnl.gov) for further
I primer: -28M13 rev2 from Amersham
I primer sequence stop: 262.
Location/Qualifiers
                                                                                                        lia; Eutheria;
ases 1 to 373)
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ilarity 42.9%;
Conservative 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:5585990"
/db_xref="taxon:9606"
/clone="IMAGE:682670"
/clone_lib="NCI_CGAP_GCB]
                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="germinal cent
/lab_host="DH10B"
/note="VAC+-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.ncbi.nlm.nih.gov/ncicgap.
r Institute, Cancer Genome Anatomy Project
                                                                                                          Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae
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.5; Mismatches
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L. Nature 377 (6547 Suppl), 3-174 (1995)
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Contact: Kerlavage,
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
For clone availability, additional sequence and expression for clone availability additional sequence and expression information related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to this EST, please check the TIGR Human formation related to the TIGR Human formation re
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    Jordan
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/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; S
    University
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                                               University Genomics
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Kozak, D.L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Frasser, C.M. and Venter, J.C.
Frasser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
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9712
                                                                                   Other_ESTs: THC1714;
Contact: Kerlavage,
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4 656 4293
dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
Institute for Genomic Research
Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX2J20"
/clone_lib="tomato root during/after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="root"
/tissue_type="root"
/dev_stage="plants during and after fruit-set"
/dev_stage="plants during and after fruit-set"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Si
Site_
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Pred. No. 36;
7; Mismatches 45
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                                                                                                                                                                                                                                               NCI-CGAP http://www....
National Cancer Institute, Cancer
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version rep
Contact: Robert Strausbergenih.gov
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free thromage Consortium (info@image.llnl.gov) for possible reversed clone: similarity on worked primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59
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Mammalia; Eutheria;
1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW628807 256 bp mRNA EST 31-MAR-2000 h140b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974735 3' similar to SW:MCL1_HUMAN Q07820 INDUCED MYELOID LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL-1.; mRNA sequence. AW628807.1 GI:7375518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Similarity 56.2%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2974735"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                                                                                                              1 to 256)
http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Institute, Cancer Genome Anatomy
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/tissue_type="bone marrow"
/dev_stage="adult"
/note="Vector: pBluescript
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/db_xref="ATCC (inhost):122003"
/db_xref="taxon:9606"
/clone_lib="Bone marrow"
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Primates;
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Pred. No. 38;
9; Mismatches
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Catarrhini;
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
Possible reversed clone: similarity on wrong strand
Insert Length: 2462 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 248.
Location/Qualifiers
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4444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 276)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, I Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marzersons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. Wilson, R.
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Eukaryota;
Mammalia; E
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Similarity 56.2%;
27; Conservative
WashU-Merck EST Project
blished (1995)
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ell.sl Soares retina N2b4HR Homo
E:219692 3' similar to SP:A47476
UCT HOMOLOG - ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Ington University School of Medicine
Forest Park Parkway, Box 8501, St. 1
314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
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1 to 276)
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Primates;
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Pred. No. 38;
9; Mismatches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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/db_xref="taxon:9606"
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M.Fatima Bonaldo. "
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IMAGE:146
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EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
Seq primer: -40m13 fwd. ET from Amersham
Location/Qualifiers
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2.467838 3' similar to SW:MCL1_HUMAN Q07820 INDUCED MYELOID
2.A CELL DIFFERENTIATION PROTEIN MCL-1. [1] ;, mRNA sequence
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/db_xref="taxon:9606"
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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29 24.6 19.4 2089 2 US-08-552-142A-1
30 24.6 19.4 2089 2 US-08-910-973-1
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38 24.4 19.2 32 3 US-08-306-691B-42
39 24.2 19.1 2325 4 US-08-32-766A-11
40 24.2 19.1 3337 1 US-08-072-610-1
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44 24.2 19.1 246240 3 US-08-724-394A-22
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58 Sequence 21, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 25, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 20, Appli Sequence 20, Appli Sequence 21, Appli Sequence 2
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ALIGNMENTS

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RESULT 2
US-08-077-848A-1/c
Sequence 1, Application US/08077848A
Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHIN ITLE OF INVENTION: POLYPEPTIDE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & STREET: 1880 Century Park East, CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-226-568-18/c
Sequence 18, Application US/09226568
Patent No. 6001992
GENERAL INFORMATION:
APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No
FILE REFERENCE: ISPH-0337
CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 3934
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Description of Artificial S
FORMATION: Sequence
                                                                                                                                                                                                                                                         22.7%;
ilarity 56.2%;
Conservative
                                                                                                                                                                                                                                                                                                                     Score 28.8; DE Pred. No. 0.4; 9; Mismatches
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                                                         Suite 5
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COUNTRY: 21P: 90

90067

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LOCATION: 61.1110;
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-077-848A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/077
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2
REFERENCE/DOCKET NUMBER: PD-2
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09211640 Patent No. 6020466 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                         ZIP: YUUU,

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Verent Computer Application Data:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTITITLE OF INVENTION: POLY NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: Spensley House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                         STREET: 1000
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                     STATE: Cali
COUNTRY: US
ZIP: 90067
                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        -640-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
27; Conserv
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                                                                                                                                                                                                        USA
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16-JUN-1993
                                                                                                                                                                                                                                                                                                                                              Ruth W.
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amino aci
acid 227
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                     08/441,375
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227 - A; when nucleotide
V."
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                                                                                                                    Version
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NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2
REFERENCE/DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
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COTHER INFORMATION: /
OTHER INFORMATION: a
OTHER INFORMATION: a
COTHER INFORMATION: a
S-09-211-640-1
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE
TITLE OF INVENTION: MCL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT I
NAME: Haile,
REGISTRATION N
REFERENCE/DOCK
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03547
FILING DATE: 31-MAR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                NAME: Wetherell, Jr., Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD-2845
RELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE
                                                                                                                                                                                                                                                                                                                            STATE: Calificountry: USA ZIP: 90067
COMPUTER READAB MEDIUM TYPE:
                                                                                                   INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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        MOLECULE TYPE:
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                        LENGTH: 3946
TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
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California
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1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                  DABLE FORM:
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                             linear
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             DNA (genomic)
                                         single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "When nucleotide 740 = C, amino acid 227 = A; when nucleotide acid 227 = V."
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pred. No. 0.4;
9; Mismatches
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LENGTH: 2488 ba
TYPE: nucleic a
STRANDEDNESS: 5
TOPOLOGY: linea
MOLECULE TYPE: DN
US-08-279-270A-2
RESULT 6
US-08-484-993B-9
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COTHER INFORMATION: /

COTHER INFORMATION: A.

COTHER INFORMATION: A.

PCT-US94-03547-1
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,270A
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSH:173-
TELECOMMUNICATION INFORMATION:
TELEFHONE: 512/320-7200
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
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US-08-279
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                                                                                           Query Match 21.3%;
Best Local Similarity 46.5%;
Matches 20; Conservative
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Duvic, Madeleine
APPLICANT: Schroeder, Wanda T.
TITLE OF INVENTION: Epidermal State of INVENTION: Thereof
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Duristreet: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5691460
GENERAL INFORMATION:
                                                 1416
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ce 2, Application
No. 5691460
                                          CTTCCTGTCTCTGTCTGTCCACCTCCTCCTCTTCCTCTCC
                                                     h 22.7%;
Similarity 56.2%;
27; Conservative
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                                                                                                                                                                                    linear
                                                                                                                                                                     DNA (genomic)
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                                                                                                                                                                                             single
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                                                                                             13;
                                                                                         Score 27; DB 2
Pred. No. 1.5;
3; Mismatches
                                                                                                                                                                                                                                                                                            UTSH:173--1/MAY
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                                                                                                                 Length
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                                                                                                                 2488;
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; LOCATION:
US-08-484-993B-9
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Best Loc
Matches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 3174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08484993B Patent No. 5837497 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
   1670
                                                           1610
                                                                                                                                                                                                                                 CELL TY FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 6060
COMPUTER REA
MEDIUM TYP
COMPUTER:
OPERATING
SOFTWARE:
                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B
FILING DATE: 09-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                               Local
                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                    ORGANISM: Canis fam. DEVELOPMENTAL STAGE: HAPLOTYPE: Diploidy
                                                                                                                                                                                                                                                          HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                               CCACTTGCCTTAATCCTGC
                         ccuccucucccucuccggc 118
                                                                                                              20.6%;
Similarity 39.2%;
31; Conservative 1:
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READABLE FORM:
I TYPE: Floppy disk
IER: IBM PC compatible
FING SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION:
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206..2353
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Hsu, Kuang T.
Podolski, Joseph S.
FENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                                                            Oocyte
                                                                                                                                                                                                                                                           Ovary
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                                                                                                                                                                                                                                                                                      Juvenile
1688
                                                                                                            Score 26.2; D
Pred. No. 2.8;
15; Mismatches
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                                                                                                                                       Length
                                                                                                           Indels
                                                                                                                                      2381;
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                                                                                                       Gaps
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RESULT

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; NAME/KEY:
; LOCATION:
US-08-484-158B-9
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                       Qy
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ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 3279
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,223
FILING DATE: 09-NOV-93
PRIOR APPLICATION NUMBER: 08/012,990
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
APPLICATION NUMBER: 07/973,341
TITTING DATE: 09-NOV-92
                                                                Best
                                                   Matches
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                                                                          Query
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                          STRANDEDNESS: dou
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                      ORIGINAL SOURCE: ORGANISM: Can
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 1610
                                                                                                                                                         FEATURE
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                                                   Match
Local Similarity
Les 31; Conser
                                                                                                                                                                                  HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                          DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                           LENGTH:
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SENSE:
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                                                                                                                                                                       TYPE:
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Podolski,
                                                  20.6%; illarity 39.2%; Conservative 1
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                                                     Score 26.2; DE Pred. No. 2.8; 5; Mismatches
                                                     Pred.
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RESULT 8
US-08-484-596A-9
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                                                                ; LOCATION US-08-484-596A-1
              Query
Best I
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SEQUENCE C
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FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
  Matches
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COMPUTER READABLE
MEDIUM TYPE: FI
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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ORIGINAL S
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                                                                                           FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
JRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                    NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                HAPLOTYPE
TISSUE TY
                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                  ORGANISM: Canis familiaris
DEVELOPMENTAL STAGE: Juven
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
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TOPOLOGY: li
              Local
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5. 5981228
INFORMATION:
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HONE: 312/474-6653
AX: 312/474-0448
: 25-3856
ON FOR SEQ ID NO: 9:
E CHARACTERISTICS:
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     31;
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20.6%;
Similarity 39.2%;
%1; Conservative 1:
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EQUENCES:
NCE ADDRES
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Podolski, Joseph S.
ENTION: Materials and Methods
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    Score 26.2; DB; Pred. No. 2.8; 15; Mismatches
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                                  DB 4;
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                                 Length 2381;
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NAME: Clough, David REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 3174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-08-480-150A-9
; Sequence 9, App
    Query Match 20. Best Local Similarity 39. Matches 31; Conservative
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APPLICATION NUMBER: US/08/480,15
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,22
FILING DATE: 09-NOV-1993
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION NUMBER: 07/973,341
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Canis familia
DEVELOPMENTAL STAGE: Ju
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
                                                                   NAME/KEY:
LOCATION:
480-150A-9
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SOFTWARE:
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2: Illinois
RY: United
60606-6402
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SYSTEM: P
Patentin
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Podolski, Joseph
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00 Sears To
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07-JUN-1995
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                 20.6%;
39.2%;
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   ore 26.2; Died. No. 2.8; Mismatches
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                          Length
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US-08-458-731-9
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Patent No
GENERAL
                                                                                                                                                                                                                                                                                           INFORMATION SEQUENCE C
                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
TELEPHONE: 312/474-6653
TELEPHONE: 312/474-0448
TELEFAX: 312/474-0448
TELEX: 25-3856
TNFORMATION FOR CED ID NO. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,731
                                                                                                                                                                                 ANTI-SENSE:
ORIGINAL SO
ORGANISM:
                                                                                                                FEATURE:
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CORRESPOND
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                                                                                                                          HAPLOTYPE:
TISSUE TYPE
CELL TYPE:
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                                                                                                                                   ORGANISM: Canis familiaris
DEVELOPMENTAL STAGE: Juven:
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                TYPE:
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STREET: 63
CITY: Chic
STATE: Ill
COUNTRY: U
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20.6%;
Similarity 39.2%;
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CHARACTERISTICS:

1: 2381 base pairs
nucleic acid
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DENCE ADDRES
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Hsu, Kuang T.
Podolski, Joseph S.
INVENTION: Materials and Methods
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)O Sears Tower, 233 South Wacker Drive
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09-NOV-1993
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Score 26.2; D Pred. No. 2.8; 15; Mismatches

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US-08-149-223A-9
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                                                                                                            US-08-149-223A-9
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Query Match
Best_Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FULL MATERIAL MATER
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,223A
FILING DATE: 09-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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COMPUTER READABLE
MEDIUM TYPE: F:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: United &
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE: ORGANISM: Can
                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                  HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                 ORGANISM: Canis familiaris
DEVELOPMENTAL STAGE: Juven
                                                                                                                                                                      NAME/KEY:
                                                                                                                                          OCATION:
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Podolski,
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-vi, Joseph
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Similarity

RESULT

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; TOPOLOGY: linear; MOLECULE TYPE: CDN; HYPOTHETICAL: NO; ANTI-SENSE: YES
US-08-480-552-18
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vei
SOFTWARE: PatentIn Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,552
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/033,086
FILING DATE: 09 MAR 1993
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 93,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9110
TELEPAX: 617/345-9111
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
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APPLICANT: Gudkov
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE
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 1236
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CITY: 1
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Similarity 36.5%;
27; Conservative
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INVENTION: Genes And Genetic Elements Associated
INVENTION: With Sensitivity To Chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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: Allegretti & Witcoff, Ltd.
75 State Street
                  cggccggga
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                                                                                             ; Score 26; DB 1; Pred. No. 3.3; 17; Mismatches
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                                                                                                                        DB 1;
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                                                                                                                         Length 2389;
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RESULT 14
US-09-235-546-4/c
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          Patent No. 6043340
GENERAL INFORMATION:
APPLICANT: Gudkov, And
APPLICANT: RON1nson,
TITLE OF INVENTION: A:
TITLE OF INVENTION: TO
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,38
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,38
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5866327nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                Query Ma
Best Loc
Matches
                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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TITLE OF INVENTION: A
TITLE OF INVENTION: TO
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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                                                                                                               4, Application 5. 6043340
                                                                                                                                                                                                                                                                                                           Similarity 36. 27; Conservative
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on, Igor B.
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: To Chemotherapeutic I
                                                    Association
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                                      Ociation of Kinesin with Chemotherapeutic Drugs
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Witcoff,
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Mismatches
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RESULT 15
US-08-929-208-18/c
; Sequence 18, Application US/08929208
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; HYPOTHETICAL:
US-09-235-546-4
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
APPLICATION NUMBER: US/08/486,382
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6043340nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTECHIE TYPE: CDNA
CURRENT APPLICATION NUMBER: US/no formation Date:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: 1
STATE:
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ZENTION: With Sensitivity To Chemotherapeutic DEQUENCES: 22
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,552
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 93,354
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9100
TELEFAX: 617/345-9111
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk -. This Drosophila melanogast
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
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Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pagelobacli.
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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

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/clone_lib="RPCI-98"
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                                                   - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://haronac.mod.buffslo.adu/Aronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.bac.haronachila.ba
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="RPCI-98"
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/clone_lib="RPCI-98"
/clone="BACR15N22"
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/plasmid="pBeloBAC11"
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone-"BACN03M23"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila DNA provided by the BDGP from the pland EST libraries. A more detailed description of the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

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/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - thtp://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Direct Submission

Submitted (23-JUL-1999) Genoscope

BP 191 91006 EVRY cedex - FRANCE |

- Web : www.genoscope.cns.fr)
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Similarity 22.9%;
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Submitted (02-JUN-1999)
BP 191 91006 EVRY cedex
- Web : www.genoscope.cu
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/db_xref="taxon:7227"
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/clone="BACN16G14"
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Drosophila melanogaster genome survey sequence SP6 end of BAC
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fly), genomic survey sequence.
AL098851
AL098851.1 GI:5610462
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Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/clone_lib="RPCI-98"
/clone="BACR14B21"
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Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Collaboration of this BAC-end sequence was carried out as part of a The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila nelanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

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Drosophila melanogaster genome survey sequence TET3 end of BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

N AL056652
AL056652.1 GI:4932342
GSS.
fruit fly.
SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Endopterygota; Diptera; Brachycera; Endopterygota; Diptera; Brachycera; Endopterygota; Diptera; Brachycera; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/clone_lib-"DrosBAC"
/clone-"BACN03K12"
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Direct Submission

L Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBeeloBAC11.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN15A09"
/note="end: T7"
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    Centre National de Sequencage
(E-mail : seqref@genoscope.cns.fr

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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                               On Mar 12, 1999 this sequence version Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                          Seq I
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Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher |
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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/clone_lib="NCI_CGAP_Kid8"
/tissue_type="renal cell tum
/lab_host="DH108"
/note="Organ: kidney; Vector
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Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2345012.TF
Contact: Mark Adams
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Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: M13 Reverse
Class: BAC ends.
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/clone="2345012"
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/note="Vector: pBeloBAC11
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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M Reticuloendotheliosis virus

Viruses; Retroid viruses; Retroviridae; Mammalian tyl
retroviruses; 3-Reticuloendotheliosis virus group.

1 (bases 1 to 578)
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Gabus-Darlix,C. and Darlix,J.
Gabus-Darlix,C. and Darlix,J.
Patent: WO 9849334-A 05-NOV-1998;
Patent: WO 9849334-A 05-NOV-1998;
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HUMTRK4A
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AC023789_0
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                                                                                                                                 ; Score 127; D pred. No. 2.8e 36; Mismatches
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L08246 Human myelo

I15824 Sequence 1

AL023797 Streptomy

AC010380 Homo sapi

AC0103406 Mouse chr

AC053497 Homo sapi

AL137219 Homo sapi

AC018744 Oryza sat

M55337 Human oncog

AL138650 Arabidops

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AC004125 Homo sapi

AC004125 Homo sapi

AL049628 Streptomy

AL049628 Streptomy

AP000478 Homo sapi

AC012409 Homo sapi

M69065 Herpes simp

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Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 3-Reticuloendotheliosis virus group.
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Fowlpox virus
Viruses; dsDNA viruses,
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/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE
/db_xref="taxon:11636"
225 c 260 g 265 t
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                                                                         Ltd, Castle
EcoRI/PstI 4
fragment
                                                                                                          /strain="S (standard vaccine strain)"
/db_xref="taxon:10261"
/note="standard vaccine strain from Cyanamid-Webster
/td, Castle Hill, New South Wales, Australia.
EcoRI/PstI 4.3kb fragment from the 9.8kb PstI genome
49. .90
/note=
                                                    integrated reticuloendotheliosis
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integration site; proving
Spleen necrosis virus
Spleen necrosis virus
Viruses; Retroid viruses
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Similarity 70.9%;
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/codon_start=1
/product="gag"
/product="gag"
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GCKPTGPSKVLLASQKVNPRRPVLPSAPESPPRMRRAQFLDERPLSPAPAPPPYPEV
PFTTSDLYNWENQNPSFSQAPDEVISLLESVFYTHPDTWDDCQQLLRTLFTTEERERV
RTESRREVRNDQGVQVTDEREIEAQFPATRPDWDPNTGRGNUNLERYRQILLRGLRAA
PDIRKKIQKIDGFQGKSLSELVAIAQKVFDQREDPAKATHELTQKMAKVLLAQESRAE
ARKPTNLSKITEVRQGADESPTAYLERLYQAYRTWSPIDPRAPENQAAIVIQFVSQSA
RGSKKTPPGKGRPPLGKNQCAYCKEEGHWKKNCPKLVSGATPVLVEELQ"
ARGSKKTPPGKGRPPLGKNQCAYCKEEGHWKKNCPKLVSGATPVLVEELQ"
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/gene="pro/pol"
/Codon_start=1
/product="protease/polymerase"
/product="protease/polymerase/polymerase/polymerase/polymerase/polymerase/polymerase/polymerase/polymerase/polymerase/polymeras
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/gene="gag"
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/gene="gag"
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CLEGSCTVNVNLGDRQ.:SDNISESSGFLMDVNTDHVIDTKYVGLFITKIKVDAHVFYG
QNVIMFPEKNLFSQTN.:PNFILYDITVQDRNVLLLITSKYIYNLCDDKYYDIFELKYL
VDNCKLPMPLIPLSKYDFTFTDLSVIKSENVKTVLSKVHTSMKSYYNNDTSLPVAVKV
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Shimotohno, K., Mizutani, S. and Te
Sequence of retrovirus provirus
transposable elements
Nature 285 (5766), 550-554 (1980)
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2 (bases 1 to 1530)
Q'Rear, J.J. and Temin, H.M.
Spontaneous changes in nucleotide
necrosis virus, an avian retrovir
Proc. Natl. Acad. Sci. U.S.A. 79
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The meaning of the substitution a
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Intaneous changes in nucleotide
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/db_xref="GI:61758"
/db_xref="GI:61758"
/db_xref="SWISS-PROT:P03342"
/translation="MGQAGSKGLLTPLECILKNFSDFKKRAGDYGEDVDSFALRKLCE
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GCKPHRTSKVLLASQKVNPRRPVLPSAPESPPRIRRAQFLDERPLSPAPAPPPPYPEV
SAIVEDTREGQQPDSTVMTSPPHTRSGLEFGAQGPSGMYPLRETGERDMTGRPMRTYV
PFTTSDLYNWKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER
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Similarity 70.1%;
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 22, 2000 this sequence version replaced gi:7242470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 147679 bases at least Q40
Consensus quality: 158044 bases at least Q30
Consensus quality: 164046 bases at least Q20
Insert size: 169678; sum-of-contigs
Insert size: 185740; 5.2% error; agarose-fp
Quality coverage: 2.78x in Q20 bases; sum-of-contigs Quality
coverage: 2.54x in Q20 bases; agarose-fp
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Center code: SC
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Eutheria; Primates;
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Mismatches 4;
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/note="assembly_fragment:00181
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32105. .33672
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/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-40A7"
/clone_lib="RPCI-11.1"
1. .2207
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vector_side:left"
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misc_feature

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AUTHORS
TITLE
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E 1 (bases 1 to 187155)

S Plumb, B.

Direct Submission

L Submitted (11-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in that the sequence may change as work continues. The understanding be contaminated with foreign sequence from E.coli, yeast, vector, segments. Contig_ID: 00010 Length: 5345bp
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Homo sapiens chromosome s
SEQUENCING IN PROGRESS **
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AL160271.1 GI:7242465
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Catarrhini; Hominidae;
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Contig_ID: 00032 Length: 1329p
Contig_ID: 000164 Length: 2017bp
Contig_ID: 00117 Length: 2018bp
Contig_ID: 00119 Length: 3917bp
Contig_ID: 00129 Length: 3761bp
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9446: contig c
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21847: contig c
8 22647: gap of
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6 33351: contig c
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Similarity 37.5%;
33; Conservative
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
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entific Inst.,
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TTGCCCTGCCTGCCTCTCTG 38142
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IRWGQPFRLRHITTGMYLALNDDEGLVMLDREKSDTTSSAFCFRASKELKEKQDSTLK
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Inst., via Olgettina 58, I-20132, Milano, ITALY
Location/Qualifiers
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STAGDTHLGGEDFDNRLVNHFAEEFKRYKKDLRSNPRALRRLTAAERAKRTLSSY
IAGINVLRIINEPTAAALAYGLDKNLKGERNVLIFDLGGTEDVSLITIDEGSLFEVR
EASLEIDALYEGHDFYSKVSRAFFEELCGDLFRNTLEPVERALKDAKMDKSQIHDIYL
UVAPLSLGIETAGGVMTKLIERNSRIPCKQSKTFTTYADAPAILSGDKSSEIKDVLLV
NVLGTFDLTGVPPAPRGVPKIDVTFDLDANGILNVTAKEQGTGNAKNITIKNDKGRL
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/db_xref="taxon:7227"
/chromosome="3"
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y, Wellington Rd, Clayton, Vic 3168, Australia
Cocation/Qualifiers
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Pphydroidea; Drosophilidae; Drosophila.
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HTG; H..
fruit fly.
Drosophila mela.
Eukaryota; Metazoa,
Eukaryota; Neoptera; E..
Pterygota; Neoptera; E..
Muscomorpha; Ephydroidea; L.
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Muscomorpha; Ephydroidea; L.
Sadams, M. and Venter, J.C.
Direct Submission
For More Submission
For More information on this record e-mail to form or or information on this record e-mail to form or the finished sequence will be replaced
* This sequence will be replaced
* by the finished sequence as soon as it is averaged the accession number will be preserved.
Location/Qualifiers
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Tanism="Drosophila melanogaster"
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SEQUENCE, 19 unordered pi
AC022005
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HTG; HTGS_PHASE1.
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24; Conservative
                                                         Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 165821)

1 (bases 1 to 165821)

1 (bases 1 to 165821)

Wang, J., Hu, S., Dong, W., Zhang, X., Wang, X., Zhang, Y., Zhang, H.
Wang, J., Hu, S., Dong, W., Zhang, X., Wang, X., Cheng, C., Wang, Y., Bao, W., Yu, B., Fan, H., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Niu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J. and Yang, H.
Chromosome 3p genomic sequence
2 (bases Wang,J., Liu,B., I
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Eukaryota; M
                                                Unpublished
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   Dong, W., Zhang, X., Wang, X., Zhang, Y., Sun, Y., Wu, Q., Wang, H., Yang, X., Chen Li, T., Zhang, H., Liu, N., Wu, D., Yu, B.,
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Catarrhini; Hominidae; Homo.
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YGGYSSSVHKQNLYVVSFPIIFLFNVLRSLIYQLFCIFRYLYGASTKVIYRPHRRDCN
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Pterygota; Neoptera; Endopterygota; Diptera; Drosophila.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
Rockville, MD, USA
This sequence was identified as CDM:10213304 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* Location/Qualifiers
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Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-1070N10
of RPCI-11 library from chromosome 14 of Homo sapiens (Human),
                                                                                       Submitted (31-MAR-2000) to the EMBL/GenBank/DDBJ databases on Apr 3, 2000 this sequence version replaced gi:6981914.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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/db_xref="taxon:7227"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="matching EMBL:Z16446; RHdb:RH95830; RH
the e-PCR software (G. Schuler)"

44289. .44410

/note="matching EMBL:AA857911; RHdb:RH93740;
dbSTS:STS66733; Identified using the e-PCR software
Schuler)"

55614. .55842

/note="matching EMBL:T72567; RHdb:RH93712; db:
55637. .55816

/note="matching EMBL:T72567; RHdb:RH44140; RH6
Schuler)"

156244. .156393

/note="matching EMBL:T72567; RHdb:RH44140; RH6
Schuler)"

156244. .156393

/note="matching EMBL:AA129468; RHdb:RH48023;
Schuler)"

181390. .181580

/note="matching EMBL:R68409; RHdb:RH48023;
Schuler)"

181390. .181580

/note="matching EMBL:R68409; RHdb:RH45107; dbS
Identified using the e-PCR software (G. Schule
184384. .184606

/note="matching EMBL:T96687; RHdb:RH45337; dbS
Identified using the e-PCR software (G. Schule
189245. .189443

/note="matching EMBL:R70888; RHdb:RH77821; dbS
Identified using the e-PCR software (G. Schule
190705. .190868

/note="matching EMBL:AA856757; RHdb:RH98896;
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V63778 stand V63778; 17-MAR-1999 Sequence der Reticuloendo

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			0;	P						1 8 + 0 r c	L H C C C	-1 qe	

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KW type C retrovirus; internal ribosome entry site; IRES; encapsidation;
KW retroviral vector; gene therapy; ss.

SR Reticuloendotheliosis virus.

PN FR2762615-A1.

PN FR2762615-A1.

PN 30-OCT-1998.

PP 28-APR-1997; 005203.

PR (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PR WPI; 99-037487/04.

PS Expression vectors containing IRES and/or encapsidation enhancer of the pression vectors containing IRES and/or encapsidation enhancer of the present sequence is derived from the 5' end of the genomic RNA of C Retrovirus other than FMLV and MOMLV

PT Claim 5; Page 31-32; 43pp; French.

PS Claim 5; Page 31-32; 43pp; French.

CC Reticuloendotheliosis virus type A (REV-A). The specification also c for personal recombination of the genomic RNA of a type C retrovirus other than Friend murine of the genomic RNA of a type C retrovirus other than Friend murine contained a virus (FMLV) and Moloney murine leukaemia virus (MOMLV). The custom of the sequences are used as an internal ribosome entry site (IRES) c derived sequences are used as an internal ribosome entry site (IRES) c derived sequences are used as an internal ribosome entry site (IRES) c derived rector can be used for gene therapy, production of recombinant polypeptides or production of transgenic animals.

CC recombinant polypeptides or production of transgenic animals.

SQ Sequence 940 BP; 190 A; 225 C; 260 G; 265 U;
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A (CSIR) COUPART BEH, GOULD FR.

I Boyle DB, Coupar BEH, Gould FR.

RWPI; 99-167428/14.

RRPI; 99-167428/14.

Recombinant vaccine against fowlpox virus - is free of contaminant policies of recombinant vaccine against virus, used to prevent the virus of courrence in chickens of courrence in chickens or courrence in chickens or courrence an active reticuloendotheliosis virus (REV), and courrence of each active reticuloendotheliosis virus (REV), and courrence of courrence of fowlpox virus. The vaccine is used to produce a vaccine against fowlpox virus. The vaccine is used to produce a vaccine against fowlpox virus. The vaccine is used to consisted the occurrence of fowlpox virus in chickens. The chickens can be consisted at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with 1 day can be vaccinated at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a confer full length provirus of REV, and can give rise to infectious REV near full length provirus of REV, and can give rise to infected. The
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Best Local S
Matches 127
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07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
(CSIR ) COMMONWEALTH SCI & IN BOYle DB, Coupar BEH, Gould AWPI; 99-167428/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fowlpox virus (FPV S) 5' LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis vaccine; chicken; LTR; long terminal repeat; ss.
Fowlpox virus.
W09907852-Al.
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                                                                                                                                                                                                                            Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect the most cell and form provirus

Example; Page 16-17; 28pp; English.

Example; Page 16-17; 28pp; English.

C New recombination-free, highly efficient retroviral vectors

C pPO111-R1 (given in Q76038), pPO111-R2 (Q76039) and pPO111-R3

C (Q76040) were obtained by replacing the U3 region of the left

C (Q76040) were obtained by replacing the U3 region of the left

C and extension of the encapsidation region. The vectors allow

C cell-type specific gene expression and eliminate risks of

C downstream activation of cellular proto-oncogenes.

C sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences X26110-115 represent long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above. Sequence 4643 BP; 1326 A; 1015 C; 1127 G; 1175 T;
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Spleen necrosis viri

W09429437-A.

22-DEC-1994: U06415

07-JUN-1993; US-073

(UYNE-) UNIV NEW JE

Dornburg RC;

WPI; 95-036467/05.

Recombinant retrovi
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Retrovirus vector pPO111-R3.
Retrovirus; vector; pPO111-R3; spleen necrosis virus; SNV;
Retrovirus; vector; pPO111-R3; spleen necrosis virus; SNV;
cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
long terminal repeat; LTR; encapsidation; gene transfer;
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                                                                   C 076038 standard; DNA; 5528 Bp.
C 076038;
C 076038;
T 20-JUL-1995 (first entry)
E Retrovirus vector pp0111-R1; spleen necrosis virus; SNV;
W Retrovirus; CMV; intermediate-early promoter; IE promoter;
W cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
W long terminal repeat; LTR; encapsidation; gene transfer;
W gene therapy; ss.
Spleen necrosis virus.
N 09429437-A.
D 22-DEC-1994; U06415.
R 07-JUN-1993; US-073345.
R 07-JUN-1993; US-073345.
R (UYNE-) UNIV NEW JERSEY.
D 27-DEC-1994; P5-036467/05.
T Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect sexample; Page 13-14; 28pp; English.
C New recombination-free, highly efficient retroviral vectors pp0111-R1 (given in 076038), pp0111-R2 (076039) and pp0111-R3
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C 076039;
T 20-JUL-1995 (first entry)
E Retrovirus vector pP0111-R2.
W Retrovirus; vector; pP0111-R2; spleen necrosis virus; SNV;
W Cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
W gene therapy; ss.
W gene therapy; ss.
Spleen necrosis virus.
W 09429437-A.
D 23-DEC-1994.
W 09429437-A.
D 37-JUN-1994; U06415.
N 07-JUN-1993; US-073345.
N 07-JUN-1994; U06415.
N 07-JU
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Pred. No. 1.3e-29;
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5528 BP; 1265 A; 1423 C; 1457 G; 1383 7
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illarity 69.9%;
Conservative 3:
                                                                                       DNA;
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Pred. No. 1.3e-29;
3; Mismatches 4;
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mcl-1;

diagnostic;

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D 22-DEC-1994.
D 22-DEC-1994; U03547.
F 31-MAR-1994; U03547.
F 31-MAR-1994; US-077848.
R (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
Craig RW;
I Craig RW;
I Craig RW;
I Craig RW;
R P-PSDB; R68814.
R P-PSDB; R68814.
R P-PSDB; R68814.
I disorders, partic. myeloid cell leukaemia
I disorders, partic. myeloid cell leukaemia
I Disclosure; Page 46-49; 67pp; English.
DNA encoding new myeloid cell leukemia associated gene mcl
DNA encoding new myeloid cell leukemia associated gene mcl
isolated from a cDNA library prepd. from ML-1 human myelob
isolated from a cDNA library prepd. The predicted gene produ
(given in R68814) contained 350 amino acids and had a mol.
C 37.3 kDa.
Sequence 3946 BP; 1048 A; 803 C; 970 G; 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
Matches 2
                                                                                                                                                                                                                                                         T11309;
19-AUG-1996 (first entry)
19-AUG-1996 (first entry)
Allergen Alt a 12 protein encoding cDNA.
Allergen Alt a 12; allergen; epitope; in
Alt a 45; Alt a 12; allergen; energy; ds.
detection; immunotolerance; anergy; ds.
alternaria alternata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic;
Homo sapiens.
Key
                                                                                                                                                            Alternaria alternata.
AT9402038-A.
15-NOV-1995.
02-NOV-1994; 002038.
02-NOV-1994; AT-002038.
(BIOM-) BIOMAY PRODN & HANDEI Achatz G, Breitenbach M, Et Oberkofler H, Prillinger H, WPI; 96-040555/05.
P-PSDB; R88692.
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They can also deter
their stimulatory (
can also be used the
T lymphocytes.
Sequence 333 BP;
                          Recombinant DNA encoding allergens of Alternaria alternata - useful in diagnosis and treatment of A. alternata allergies Claim 1; Page 14; 21pp; German.
Claim 1; Page 14; 21pp; German.
The present sequence encodes an Alt a 12 allergen protein isolated from Alternaria alternata. Peptide epitopes from Alt a 12 and Alt a 45 alternaria alternata. Peptide epitopes from Alt a 12 and in vitro detection (R88672) are useful as diagnostic reagents, e.g. for in vitro detection of allergy caused by Alt a 45 and 12 (by reaction with IgE in serum). They can also detect cellular reaction to the specified allergens (from their stimulatory or inhibitory effect on this reaction). The peptides can also be used therapeutically to induce immunotolerance or anergy of
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740
/*tag=_a
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56.2%;
ative
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          A;
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          101
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ope; immunoglobulin
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Query Match Best Local Matches

Similarity 29; Conser

21.6%; ty 47.5%; ervative 1

Score 27.4; D Pred. No. 2.2; 11; Mismatches

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Length

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Gaps

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Match

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Q45332 standard; cDNA; 2487 BP.

ID Q45332
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BT 21.NOV-1994 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New epidermal surface antigen and DNA encoding it - are useful to treat diseases such as cancer, and to detect restriction fragment regard polymorphisms on human chromosome 17 associated with auto-immune bullous diseases.

The auto-immune bullous diseases.

The claim 5; Fig 2; 89pp; English.

Colaim 5; Fig 2; 89pp; English.

Con human chromosome 17 has been isolated. The antigen is involved in continuous common of the coding sequence and ESA can be used to treat continuous endough the coding sequence and congenital bullous diseases, and cancers such as malignant schwannomas and concers such as malignant schwannomas and concers and other neural crest tissue cancers. The ESA coding sequence also provides a chromosome 17 marker, e.g. for RFLPs.

Concerned the sequence of the coding sequence also provides a chromosome 17 marker, e.g. for RFLPs.

Sequence 2487 BP; 499 A; 712 C; 722 G; 554 T;
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Best Loc
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gene therapy; probe; (
Homo sapiens.
US5691460-A.
25-NOV-1997.
22-JUL-1994; 279270.
22-JUL-1994; US-27927
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27-MAR-1998
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Similarity 46.5%; Pred. No. 5.3;
20; Conservative 13; Mismatches 10; Indels
                                                                                                                                                           8 (first entry)
idermal surface antigen.
surface antigen; treatment; diagnosis;
surface antigen; treatment; bullous pemphigoid;
bullous disease; pemphigus; bullous pemphigoid;
py; probe; detection; chromosome 17 abnormality;
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IGTCTCTCCTGTCTGTCCACCTCCTCCTCTTCCTCTCC
                                                                                                                                                                                                                                                                                                                              ndard; DNA; 2488 BP.
           279270.
US-279270.
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PD 11-MAR-1999; U18426.

PR 02-SEP-1998; U18426.

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Duvic M, Schroeder WT;

WPI; 98-017714/02.

P-PSDB; W38288.

Isolated epidermal surface antigen gene - for production antigen for diagnosis or therapy of auto:immune diserchaim 1; Columns 31-34; 28pp; English.

The present sequence encodes an epidermal surface antigen gene therapy, to generate or diagnose autoimmune busenes pemphigus or bullous pemphigoid. The ESA DNA may gene therapy, to generate nucleic acid probes or to chromosome 17 abnormalities.

Sequence 2488 BP; 499 A; 712 C; 723 G;
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X23518;
23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kidney aminopeptidase P genomic DNA fragment 2.
Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency;
prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis;
arterial stenosis; industrial protein feed; malabsorption syndrome;
proteinaceous waste degradation; additive; immunohistochemistry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9911799-A2.
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Similarity 46.5%;
20; Conservative
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                                                                                           78;
                                                               Score 27; DB; Pred. No. 12; 19; Mismatches
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auto:immune diseases,
                                                               30;
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bullous diseases,
may be used for
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Local

\$1 42;

ilarity

21.18; larity 38.28; Conservative 1

Score 26.8; D Pred. No. 5.6; Mismatches

DB 1;

Length 1760;

52;

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PT New isolated nucleic acid encoding sub-units of liver activin - procession is solated nucleic acid encoding sub-units of liver activin - procession is colored to provide the provides murine liver activin beta e polypeptide. The invention CC provides murine liver activin beta c and beta e genes. Disorders of cell CC growth or differentiation (or susceptibility to them) are diagnosed by activin gene. Disorders of haematopoiesis, erythroid differentiation, compound activiny or by detecting a mutation in the covarian follicular maturation, hormone secretion, neuronal survival, comprise sis are some conditions that can be diagnosed using the liver activin an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while consteoprosis or osteomalacia) or haematopoiesis, particularly conspound may also induce bone growth (e.g. for treating thempoinesis, particularly conspoints activin compound may also induce bone growth (e.g. for treating thempoinesis, particularly conspoints activin. Also, transgenic animals containing liver activin consteomalacia) or haematopoiesis, particularly consolitied forms) proteins, or the transgenic animals containing liver activin modulators.

Sequence 1760 BP; 390 A; 502 C; 514 G; 354 T;
Query Ma
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28-MAY-1998.
20-NOV-1997; U20882.
20-NOV-1996; US-752919.
(UNMI) UNIV MICHIGAN.
Bonadio J, Fang J;
WPI; 98-312408/27.
P-PSDB; W60619.
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V38240;
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Human live
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spermatoge
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er activin beta e polypeptide encoding cDNA.
ivin; beta c; beta e; cell differentiation; haematopoiesis;
; ovarian follicular maturation; hormone; neuronal survival;
enesis; bone; insulin; cardiac morphogenesis; osteoporosis;
cia; erythropoiesis; haemophilia; cystic fibrosis; immunoass;
disorder; transgenic; modulator; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     andard; cDNA; 1760 Bp.
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127. .
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77. .126
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77. .1129
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TTCTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTGGCCTGCCAGTA 1010

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20.6%; Score 26.2; DB 1;
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Length

Query Match

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Decorate primers given in Q70075-78.

Secontraceptive; vaccine; contraceptive; vaccine; was canis familiaris.

Particular pellucida; ZP; CZP2; contraceptive; vaccine; was canis familiaris.

Canis familiaris.

Decorposition: CORP.

Particular pellucida; ZP; CZP2; contraceptive; vaccine; was profit pellucida czp2.

Canis familiaris.

Particular pellucida; ZP; CZP2; contraceptive; vaccine; was profit pellucida czp2.

Canis familiaris.

Particular pellucida; ZP; CZP2; contraceptive; vaccine; pellucida; contraceptive; pellucida; czp2.

Particular pellucida; czp2.

Reprimers given contraceptive vaccine antigen; pellucida; czp2.

Canis familiaris.

Particular pellucida; zP; CZP2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

CZP2 DEC-1992; JP-359265.

Particular pellucida; zP; czp2; contraceptive; vaccine; pellucida; czp2.

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